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(71) Applicant *(for all designated States except US)*: FOX CHASE CANCER CENTER [US/US]; 7701 Burholme Avenue, Philadelphia, PA 19111 (US).

(72) Inventors; and
(75) Inventors/Applicants *(for US only)*: KRUH, Gary [US/US]; 241 South 6th Street #809, Philadelphia, PA 19106 (US). LEE, Kun [KR/US]; 21 Barrington Drive, Cranbury, NJ 08512 (US). BELINSKY, Martin [US/US]; 625 Parmentier Road, Warminster, PA 18974 (US). BAIN, Lisa [US/US]; 284 Penny Lane, Townville, SC 29689 (US).

(74) Agents: RIGAUT, Kathleen, D. et al.; Dann, Dorfman, Herrell and Skillman, Suite 720, 1601 Market Street, Philadelphia, PA 19103 (US).

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(54) Title: MPR–RELATED ABC TRANSPORTER ENCODING NUCLEIC ACIDS AND METHODS OF USE THEREOF

(57) Abstract

Novel human MOAT genes and their encoded proteins are provided herein. The MRP–related ABC transporters encoded by the disclosed nucleic acid sequences play a pivotal role in the efflux of pharmacologically benefical reagents from tumor cells. MOAT genes and their encoded proteins provide valuable therapeutic targets for the design of anti–cancer agents which inhibit the aberrant growth of malignant cells.

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MRP-Related ABC Transporter Encoding Nucleic Acids and Methods of Use Thereof

Pursuant to 35 U.S.C. §202(c) it is acknowledged that the U.S. Government has certain rights in the invention described herein, which was made in part with funds from the National Institutes of Health, Grant Numbers, CA63173 and CA06927.

FIELD OF THE INVENTION

The present invention relates to the fields of medicine and molecular biology. More specifically, the invention provides nucleic acid molecules and proteins encoded thereby which are involved in the development of resistance to pharmacological and chemotherapeutic agents in tumor cells.

BACKGROUND OF THE INVENTION

Several publications are referenced in this application in parentheses in order to more fully describe the state of the art to which this invention pertains. The disclosure of each of these publications is incorporated by reference herein.

P-glycoprotein, the product of the *MDR1* gene, was the first ABC transporter shown to confer resistance to cytotoxic agents. Pgp functions as an ATP-dependent efflux pump that reduces the intracellular concentration of a variety of chemotherapeutic agents by transporting them across the plasma membrane (1). The multidrug resistance phenotype associated with overexpression of Pgp

is of considerable clinical interest because natural product drugs are second only to alkylating agents in clinical utility, and many effective chemotherapeutic regimens contain more than one natural product agent. More recently, we and others have reported transfection studies indicating that MRP, another ABC family transporter, confers a multidrug resistance phenotype that includes many natural product drugs, but is distinct from the resistance phenotype associated with Pgp (2-6). MRP shares only limited amino acid identity with Pgp, and this is reflected in the different substrate specificities of the two transporters. In contrast to Pgp, MRP can transport a wide range of anionic organic conjugates, including glutathione S-conjugates (7). In addition to Pgp and MRP there may be other transporters that are involved in cytotoxic drug resistance. In the case of natural product drugs, resistant cell lines have been described that display a multidrug resistant phenotype associated with a drug accumulation deficit, but do not overexpress Pgp or MRP (8). ABC transporters have also been linked to cisplatin resistance, and several lines of evidence suggest the possibility that pumps specific for organic anions may be involved: 1) decreased cisplatin accumulation is consistently observed in cisplatin resistant cell lines (9); 2) cisplatin is conjugated to glutathione in the cell, and this anionic conjugate is toxic in an *in vitro* biochemical assay (10); and 3) biochemical studies using membrane vesicle preparations have shown that cisplatin resistant cells lines have enhanced expression of an ATP-dependent transporter of CDDP-glutathione and other glutathione S-conjugates such as the cystinyl leukotriene LTC_4 (11, 12). These data thus suggest that an organic anion transporter may contribute

to cisplatin resistance by exporting CDDP-glutathione. While MRP is an organic anion transporter, the reported drug resistance profile of MRP-transfected cells does not extend to this agent (5, 6), and to date only one cisplatin resistant cell line has been reported to overexpress MRP (13). This suggests that organic anion transporters other than MRP may contribute to cisplatin resistance. Consistent with this possibility, the canalicular multispecific organic anion transporter, cMOAT, an MRP-related transporter that functions as the major organic anion transporter in liver, has been reported to be overexpressed in cisplatin resistant cell lines (14, 15). A more direct link between cMOAT and cytotoxic drug resistance is suggested by a recent report in which transfection of a cMOAT antisense construct into a liver cancer cell line resulted in sensitization to cisplatin, daunorubicin and other cytotoxic agents (16).

Clearly, a need exists for identifying the essential components and mechanisms giving rise to drug resistance and the transport of anticancer agents out of the tumor cell. The elucidation of these mechanisms may be used to advantage for the design of efficacious chemotherapeutic agents.

SUMMARY OF THE INVENTION

This invention provides novel, biological molecules useful for identification, detection, and/or molecular characterization of components involved in the acquisition of drug resistance in tumor cells. According to one aspect of the invention, an isolated nucleic acid molecule is provided which includes a sequence encoding a protein transporter of a size between about 1300 and 1350 amino acids in length. The encoded protein, referred to herein

as MOAT-B, comprises a multi- domain structure including a tandem repeat of nucleotide binding folds appended C-terminal to a hydrophobic domain that contains several potential membrane spanning helices. Conserved Walker A and B ATP binding sites are present in each of the nucleotide binding folds.

In a preferred embodiment of the invention, an isolated nucleic acid molecule is provided that includes a cDNA encoding a human MOAT-B protein. In a particularly preferred embodiment, the human MOAT-B protein has an amino acid sequence the same as Sequence I.D. No. 2. An exemplary MOAT-B nucleic acid molecule of the invention comprises Sequence I.D. No. 1.

According to another aspect of the invention, a second isolated nucleic acid molecule is provided which includes a sequence encoding a transporter between about 1400 and 1450 amino acids. The encoded protein, referred to herein as MOAT-C contains a multi-domain structure including a tandem repeat of nucleotide binding folds appended C-terminal to a hydrophobic domain that contains several potential membrane spanning helices. Conserved Walker A and B ATP binding sites are present in each of the nucleotide binding folds. While similar in structure to MOAT-B described above, MOAT-C contains distinct sequence differences.

In a preferred embodiment of the invention, an isolated nucleic acid molecule is provided that includes a cDNA encoding a human MOAT-C protein. In a particularly preferred embodiment, the human MOAT-C protein has an amino acid sequence the same as Sequence I.D. No. 4. An exemplary MOAT-C nucleic acid molecule of the invention comprises Sequence I.D. No. 3.

According to yet another aspect of the invention, an

isolated nucleic acid molecule is provided which includes a sequence encoding a protein of a size between about 1500 and 1550 amino acids in length. The encoded protein, referred to herein as MOAT-D, contains a multidomain structure including an N-terminal hydrophobic extension which harbors five transmembrane spanning helices.

In a preferred embodiment of the invention, an isolated nucleic acid molecule is provided that includes a cDNA encoding a MOAT-D protein. In a particularly preferred embodiment, the human MOAT-D protein has an amino acid sequence the same as Sequence I.D. No. 6. An exemplary MOAT-D nucleic acid molecule of the invention comprises Sequence I.D. No. 5.

According to yet another aspect of the invention, an isolated nucleic acid molecule is provided which includes a sequence encoding a protein of a size between about 1480 and 1530 amino acids in length. The encoded protein, referred to herein as MOAT-E, contains a multidomain structure including an N-terminal hydrophobic extension which harbors several transmembrane spanning helices. While similar in structure to MOAT-D described above, MOAT-E contains distinct sequence differences.

In a preferred embodiment of the invention, an isolated nucleic acid molecule is provided that includes a cDNA encoding a MOAT-E protein. In a particularly preferred embodiment, the human MOAT-E protein has an amino acid sequence the same as Sequence I.D. No. 8. An exemplary MOAT-E nucleic acid molecule of the invention comprises Sequence I.D. No. 7.

According to another aspect of the present invention, an isolated nucleic acid molecule is provided, which has a sequence selected from the group consisting of: (1) Sequence I.D. No. 1; (2) a sequence specifically

hybridizing with preselected portions or all of the complementary strand of Sequence I.D. No. 1 comprising nucleic acids encoding amino acids 1-1154 of Sequence ID No. 2; (3) a sequence encoding preselected portions of Sequence I.D. No. 1 within nucleotides 1-3462, (4) Sequence I.D. No. 3; (5) a sequence specifically hybridizing with preselected portions or all of the complementary strand of Sequence I.D. No. 3 comprising nucleic acids encoding amino acids 1-442 of Sequence ID No. 4; (6) a sequence encoding preselected portions of Sequence I.D. No. 3 within nucleotides 1-1326, (7) Sequence I.D. No. 5; (8) a sequence specifically hybridizing with preselected portions or all of the complementary strand of Sequence I.D. No. 5 comprising nucleic acids encoding amino acids 1-1036 of Sequence ID No. 6; (9) a sequence encoding preselected portions of Sequence I.D. No. 5 within nucleotides 1-3108, (1) Sequence I.D. No. 7; (2) a sequence specifically hybridizing with preselected portions or all of the complementary strand of Sequence I.D. No. 7 comprising nucleic acids encoding amino acids 1-998 of Sequence ID No. 8; (3) a sequence encoding preselected portions of Sequence I.D. No. 7 within nucleotides 1-300.

Such partial sequences are useful as probes to identify and isolate homologues of the MOAT genes of the invention. Additionally, isolated nucleic acid sequences encoding natural allelic variants of the nucleic acids of Sequence I.D. Nos., 1, 3, 5 and 7 are also contemplated to be within the scope of the present invention. The term natural allelic variants will be defined hereinbelow.

According to another aspect of the present invention, antibodies immunologically specific for the human MOAT proteins described hereinabove are provided.

In yet another aspect of the invention, host cells comprising at least one of the MOAT encoding nucleic acids are provided. Such host cells include but are not limited to bacterial cells, fungal cells, insect cells, mammalian cells, and plant cells. Host cells overexpressing one or more of the MOAT encoding nucleic acids of the invention provide valuable research tools for assessing transport of chemotherapeutic agents out of cells. MOAT expressing cells also comprise a biological system useful in methods for identifying inhibitors of the MOAT transporters.

Another embodiment of the present invention encompasses methods for screening cells expressing MOAT encoding nucleic acids for chemotherapy resistance. Such methods will provide the clinician with data which correlates expression of a particular MOAT genes with a particular chemotherapy resistant phenotype.

Diagnostic methods are also contemplated in the present invention. Accordingly, suitable oligonucleotide probes are provided which hybridize to the nucleic acids of the invention. Such probes may be used to advantage in screening biopsy samples for the expression of particular MOAT genes. Once a tumor sample has been characterized as to the MOAT gene(s) expressed therein, inhibitors identified in the cell line screening methods described above may be administered to prevent efflux of the beneficial chemotherapeutic agents from cancer cells.

The methods of the invention may be applied to kits. An exemplary kit of the invention comprises MOAT gene specific oligonucleotide probes and/or primers, MOAT encoding DNA molecules for use as a positive control, buffers, and an instruction sheet. A kit for practicing the cell line screening method includes frozen cells

comprising the MOAT genes of the invention, suitable culture media, buffers and an instruction sheet.

In a further aspect of the invention, transgenic knockout mice are disclosed. Mice will be generated in which at least one MOAT gene has been knocked out. Such mice will provide a valuable in biological system for assessing resistance to chemotherapy in an in vivo tumor model.

Various terms relating to the biological molecules of the present invention are used hereinabove and also throughout the specification and claims. The terms "percent similarity" and "percent identity (identical)" are used as set forth in the UW GCG Sequence Analysis program (Devereux et al. NAR 12:387-397 (1984)).

With reference to nucleic acids of the invention, the term "isolated nucleic acid" is sometimes used. This term, when applied to DNA, refers to a DNA molecule that is separated from sequences with which it is immediately contiguous (in the 5' and 3' directions) in the naturally occurring genome of the organism from which it originates. For example, the "isolated nucleic acid" may comprise a DNA or cDNA molecule inserted into a vector, such as a plasmid or virus vector, or integrated into the genomic DNA of a prokaryote or eukaryote.

With respect to RNA molecules of the invention, the term "isolated nucleic acid" primarily refers to an RNA molecule encoded by an isolated DNA molecule as defined above. Alternatively, the term may refer to an RNA molecule that has been sufficiently separated from RNA molecules with which it would be associated in its natural state (i.e., in cells or tissues), such that it exists in a "substantially pure" form (the term "substantially pure" is defined below).

With respect to protein, the term "isolated protein" or "isolated and purified protein" is sometimes used herein. This term refers primarily to a protein produced by expression of an isolated nucleic acid molecule of the invention. Alternatively, this term may refer to a protein which has been sufficiently separated from other proteins with which it would naturally be associated, so as to exist in "substantially pure" form.

The term "substantially pure" refers to a preparation comprising at least 50-60% by weight the compound of interest (e.g., nucleic acid, oligonucleotide, protein, etc.). More preferably, the preparation comprises at least 75% by weight, and most preferably 90-99% by weight, the compound of interest. Purity is measured by methods appropriate for the compound of interest (e.g. chromatographic methods, agarose or polyacrylamide gel electrophoresis, HPLC analysis, and the like). With respect to antibodies of the invention, the term "immunologically specific" refers to antibodies that bind to one or more epitopes of a protein of interest (e.g., MOAT-B, MOAT-C or MOAT-D), but which do not substantially recognize and bind other molecules in a sample containing a mixed population of antigenic biological molecules.

With respect to nucleic acids and oligonucleotides, the term "specifically hybridizing" refers to the association between two single-stranded nucleotide molecules of sufficiently complementary sequence to permit such hybridization under pre-determined conditions generally used in the art (sometimes termed "substantially complementary"). When used in reference to a double stranded nucleic acid, this term is intended to signify that the double stranded nucleic acid has been subjected to denaturing conditions, as is well known to those of

skill in the art. In particular, the term refers to hybridization of an oligonucleotide with a substantially complementary sequence contained within a single-stranded DNA or RNA molecule of the invention, to the substantial exclusion of hybridization of the oligonucleotide with single-stranded nucleic acids of non-complementary sequence.

One common formula for calculating the stringency conditions required to achieve hybridization between nucleic acid molecules of a specified sequence homology (Sambrook et al., 1989):

T_m = 81.5°C + 16.6Log [Na+] + 0.41(% G+C) - 0.63 (% formamide) - 600/#bp in duplex

As an illustration of the above formula, using [Na+] = [0.368] and 50% formamide, with GC content of 42% and an average probe size of 200 bases, the T_m is 57°C. The T_m of a DNA duplex decreases by 1 - 1.5°C with every 1% decrease in homology. Thus, targets with greater than about 75% sequence identity would be observed using a hybridization temperature of 42°C. Such sequences would be considered substantially homologous to the nucleic acid sequences of the invention.

The nucleic acids, proteins, antibodies, cell lines, methods, and kits of the present invention may be used to advantage to identify targets for the development of novel agents which inhibit the aberrant transport of cytoxic agents out of tumor cells. The transgenic mice of the invention may be used an in vivo model for chemotherapy resistance.

The human MOAT molecules methods and kits described above may also be used as research tools and will facilitate the elucidation of the mechanism by which tumor

cells acquire a drug resistant phenotype.

BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows the predicted structure of MOAT-B and comparison with human MRP. The vertical lines indicate identical amino acids and the vertical dots indicate conserved amino acids. Gaps are indicated by periods. The overbars indicate potential transmembrane spanning segments as predicted by the TMAP program. The first and second nucleotide binding folds (NBF 1 and NBF 2) are indicated by horizontal arrows. The C-terminal 34 amino acids (residues 1291 - 1325) are replaced in the second class of MOAT-B cDNA clones by the following amino acids: ILQKKLSTYWSH. The Alignment was performed using the GAP program (gap weight 3.0, length weight 0.1) in the Genetics Computer Group Package. H. MRP: human MRP.

Figures 2A and 2B depict a comparison of the nucleotide binding folds and hydropathy profile of MOAT-B with those of other eukaryotic ABC transporters. Fig. 1A shows the comparison of the nucleotide binding folds of MOAT-B. Amino acids that are identical to those of MOAT-B are shaded, and gaps are indicated by periods. Walker A and B motifs, and the ABC transporter family signature sequence C, are underlined. Amino acid positions are indicated to the right. Amino acid sequences were aligned using the PILEUP program (gap weight 3.0, length weight 0.1) in the Genetics Computer Group Package. Fig. 1B shows a comparison of the MOAT-B hydropathy profile. To facilitate comparison, the proteins are aligned so that the N-terminal nucleotide binding folds (NBF) are roughly in register. NBF's are indicated by bars. Values above

and below the horizontal lines indicate hydrophobic and hydrophilic regions, respectively. Hydrophobicity plots were generated using the Kyte-Doolittle algorithm with a window of 7 residues. The transporters shown are: human multidrug-associated protein, H. MRP (P33529); human multispecific organic anion transporter, H. MOAT (U63970); Saccharomyces cerevisiae yeast cadmium factor 1, S. YCF1 (P39109); rat sulfonylurea receptor, R. SUR (Q09427); human cystic fibrosis transmembrane conductance regulator, H. CFTR (M28668); Leishmania P-glycoprotein, L. PgpA (P21441) and human mdr1 gene product, H. MDR1 (P08183). Accession numbers are shown in parentheses.

Figure 3 is a Northern blot showing the tissue distribution of MOAT-B transcript. Membranes containing poly (A)+ RNA prepared from human tissues were hybridized with a radiolabeled MOAT-B or GAPDH probe. Top panels show MOAT-B transcript and bottom panels show the control GAPDH transcript. Arrows indicate the position of MOAT-B transcript. Prolonged exposure of the film revealed a low level signal in liver.

Figure 4 shows the chromosomal localization of the gene encoding *MOAT-B*. Human metaphase spreads were hybridized with a biotin-labeled MOAT-B cDNA probe and detected by FITC-conjugated avidin. Hybridization signals at chromosome 13q32 in two metaphase spreads are indicated by arrows. The inset shows paired hybridization signals at band q32 of chromosome 13 from three other metaphase spreads.

Figures 5A and 5B show the predicted structures of MOAT-C and MOAT-D. Fig. 5A presents the structure of

MOAT-C. Fig. 5B shows the structure of MOAT-D. Numbered overbars indicate potential transmembrane spanning helices. Horizontal arrows indicate the positions of the amino terminal (NBF1) and C-terminal (NBF2) nucleotide binding folds. Walker A and B motifs, and the ABC transporter family signature sequence C are underlined. Bullets indicate the positions of potential N-linked glycosylation sites that are conserved with previously reported N-glycosylation sites in MRP. The indicated MOAT-C transmembrane spanning helices were predicted using the TMAP program and an input alignment of MOAT-B and MOAT-C. The indicated MOAT-D transmembrane helices are based upon inspection of an alignment with MRP.

Figures 6A and 6B show a comparison of the nucleotide binding folds and hydropathy profiles of MOAT-C and MOAT-D with those of other related ABC transporters. Fig. 6A depicts the comparison of the nucleotide binding folds. The alignment was produced using the PILEUP command (gap weight 3.0, length weight 0.1) in the Genetics Computer Group Package Version 9.1. Amino acid positions conserved in at least 4 of the 8 proteins are shaded. Periods indicate gaps in the alignment. Walker A and B, and the ABC transporter family signature sequence C are indicated by underbars. Fig. 6A shows the comparison of hydropathy profiles. To facilitate comparisons, gaps were introduced at the N-termini of some proteins in order to bring the first nucleotide binding folds into register. Nucleotide binding folds are indicated by bars. Values above and below the horizontal lines indicate hydrophobic and hydrophilic regions, respectively. Hydrophobicity plots were generated using the Kyte-Doolittle algorithm with a window of 7 residues. Accession numbers are as follows:

MRP, P33529; cMOAT, U63970, SUR, Q09428; CFTR, P-13569; MDR1, P08183.

Figure 7 is a Northern blot showing the tissue distribution of MOAT-C and MOAT-D transcripts. Blots containing poly A+ RNA prepared from various human tissues were hybridized with MOAT-C, MOAT-D and actin probes. Arrows indicate the position of the MOAT-C (top panel) and MOAT-D (middle panel) transcripts. The bottom panel shows the control actin transcript.

Figures 8A and 8B show the chromosomal localization of the *MOAT-C* and *MOAT-D* genes. Human metaphase spreads were hybridized with a biotin-labeled MOAT-C and MOAT-D cDNA probes and detected by FITC-conjugated avidin. Fig. 8A shows the localization of *MOAT-C*. Hybridization signals at chromosome 3q27 in two metaphase spreads are indicated by arrows (top). The inset shows paired hybridization signals at band q27 of chromosome 3 from three other metaphase spreads. Fig. 8B shows the localization of *MOAT-D*. Hybridization signals at chromosome 17q21-22 in two metaphase spreads are indicated by arrows (top). The inset shows paired hybridization signals at band q21-22 of chromosome 17 from three other metaphase spreads.

Figure 9 shows predicted amino acid sequence of MOAT-E. Also shown are the location of the potential transmembrane helices (overbars), the potential N-glycosylation site (black dot) and the two nucleotide binding folds (NBF1 and NBF2). Walker A and B motifs, as well as the signature C motif of ABC transporters, are also indicated.

Figure 10 shows a comparison of the hydropathy profile of MOAT-E with other members of the MRP-cMOAT subfamily. The profile reveals that MOAT-E has a hydrophobic N-terminal segment which is absent in MOAT-B and MOAT-C.

Figure 11 is a RNA blot which reveals that MOAT-E is expressed only in the liver and the kidney, suggesting that MOAT-E may participate in the excretion of substances into urine and bile. The lower panel shows hybridization of an actin probe to assess RNA loading.

Figures 12A-12J show the cDNA (SEQ ID NO: 1) and amino acid sequences (SEQ ID NO: 2)encoded by MOATB.

Figures 13A-13K show the cDNA (SEQ ID NO: 3) and amino acid sequences (SEQ ID NO: 4) encoded by MOATC.

Figures 14A-14K show the cDNA (SEQ ID NO: 5) and amino acid sequences (SEQ ID NO: 6) encoded by MOATD.

Figures 15A-15K show the cDNA (SEQ ID NO: 7) and amino acid sequences (SEQ ID NO: 8) encoded by MOATE.

DETAILED DESCRIPTION OF THE INVENTION

MRP and cMOAT are closely related mammalian ABC transporters that export organic anions from cells. Transfection studies have established that MRP confers resistance to natural product cytotoxic agents, and recent evidence suggests the possibility that cMOAT may contribute to cytotoxic drug resistance as well. Based upon the potential importance of these transporters in

clinical drug resistance, and their important physiological roles in the export of the amphiphilic products of phase I and phase II metabolism, we sought to identify other MRP-related transporters. Using a degenerate PCR approach, a cDNA molecule was isolated which encodes a novel ABC transporter designated herein as MOAT-B. The MOAT-B gene was mapped using fluorescence *in situ* hybridization to chromosome band 13q32. Comparison of the MOAT-B predicted protein with other transporters revealed that it is most closely related to MRP, cMOAT, and the yeast organic anion transporter YCF1. While MOAT-B is closely related to these transporters, it is distinguished by the absence of approximately 200 amino acid N-terminal hydrophobic extension that is present in MRP and cMOAT, and which is predicted to encode several transmembrane spanning segments. In addition, the MOAT-B tissue distribution is distinct from MRP and cMOAT. In contrast to MRP, which is widely expressed in most tissues, including liver, and cMOAT, whose expression is largely restricted to liver, the MOAT-B transcript is widely expressed, with particularly high levels in prostate, but is barely detectable in liver. These data indicate that MOAT-B is a ubiquitously expressed transporter that is closely related to MRP and cMOAT, and indicate that it is an organic anion pump relevant to cellular detoxification.

Three additional MRP/cMOAT-related transporters, MOAT-C, MOAT-D and MOAT-E are also disclosed herein. MOAT-C encodes a 1437 amino acid protein that is most closely related to MRP, cMOAT and MOAT-B, among eukaryotic transporters (33% - 37% identity). However, based upon amino acid identity, MOAT-C is considerably less related to MRP and cMOAT than the latter transporters are to each

other (48% identity). In addition, the MOAT-C topology is distinct from that of MRP and cMOAT in that it, like MOAT-B, lacks an N-terminal transmembrane spanning domain. MOAT-D encodes a 1530 amino acid transporter that is highly related to MRP (57% identity) and cMOAT (47% identity). MOAT-E encodes 1503 amino acid transporter that is highly related to MOAT-D, MRP and cMOAT (39-45% identity). The topology of MOAT-D and MOAT-E are quite similar to MRP and cMOAT, in that they have an N-terminal hydrophobic extension that is predicted to harbor five transmembrane spanning helices. *MOAT-C* and *MOAT-D* were mapped to chromosome bands 3q27 and 17q21-22, respectively, by fluorescence *in situ* hybridization.

The expression patterns of MOAT-C, MOAT-D and MOAT-E are distinct from those of MRP, cMOAT and MOAT-B. MOAT-C transcript is widely expressed, with highest levels in skeletal muscle, kidney and testis, but is expressed at barely detectable levels in liver and lung. MOAT-D transcript has a more restricted expression pattern, with high levels in colon, pancreas, liver and kidney. Data presented herein reveal that MOAT-E expression is restricted to liver and kidney.

Based upon degree of amino acid identity, and protein topology, the MRP-related transporters fall into two groups, with the first group consisting of MRP, cMOAT, MOAT-D and MOAT-E, and the second group consisting of MOAT-B and MOAT-C. The isolation of MOAT-C, MOAT-D and MOAT-E thus helps to define the MRP/cMOAT subfamily. The high degree of amino acid identity and topological similarity of MOAT-D and MOAT-E to MRP and cMOAT suggest that they function as organic anion transporters, and play a role in cytotoxic drug resistance. In contrast, the lower degree of amino acid identify and distinct topology

of MOAT-B and MOAT-C suggest the possibility that their substrate specificities and functions may be distinct from that of MRP, cMOAT, MOAT-D and MOAT-E.

The compositions, methods, kits and transgenic mice of the invention disclosed herein will facilitate the identification of drugs that cripple the ability of MOAT genes and proteins encoded thereby to effect the efflux of clinically beneficial pharmacological agents in malignant cells.

I. Preparation of MOAT-Encoding Nucleic Acid Molecules, MOAT Proteins, and Antibodies Thereto

A. Nucleic Acid Molecules

Nucleic acid molecules encoding the MOAT proteins of the invention may be prepared by two general methods: (1) synthesis from appropriate nucleotide triphosphates, or (2) isolation from biological sources. Both methods utilize protocols well known in the art. The availability of nucleotide sequence information, such as cDNAs having Sequence I.D. Nos. 1, 3, 5, or 7 enables preparation of an isolated nucleic acid molecule of the invention by oligonucleotide synthesis. Synthetic oligonucleotides may be prepared by the phosphoramidite method employed in the Applied Biosystems 38A DNA Synthesizer or similar devices. The resultant construct may be purified according to methods known in the art, such as high performance liquid chromatography (HPLC). Long, double-stranded polynucleotides, such as a DNA molecule of the present invention, must be synthesized in stages, due to the size limitations inherent in current oligonucleotide synthetic methods. Thus, for example, a 5 kb double-stranded molecule may be synthesized as several smaller segments of appropriate complementarity. Complementary segments thus

produced may be annealed such that each segment possesses appropriate cohesive termini for attachment of an adjacent segment. Adjacent segments may be ligated by annealing cohesive termini in the presence of DNA ligase to construct an entire 5 kb double-stranded molecule. A synthetic DNA molecule so constructed may then be cloned and amplified in an appropriate vector.

Nucleic acid sequences encoding the MOAT proteins of the invention may be isolated from appropriate biological sources using methods known in the art. In a preferred embodiment, a cDNA clone is isolated from a cDNA expression library of human origin. In an alternative embodiment, utilizing the sequence information provided by the cDNA sequence, human genomic clones encoding MOAT proteins may be isolated. Alternatively, cDNA or genomic clones having homology with MOAT-B, MOAT-C, MOAT-D or MOAT-E may be isolated from other species using oligonucleotide probes corresponding to predetermined sequences within the MOAT encoding nucleic acids.

In accordance with the present invention, nucleic acids having the appropriate level of sequence homology with the protein coding region of Sequence I.D. Nos. 1, 3, 5, and 7 may be identified by using hybridization and washing conditions of appropriate stringency. For example, hybridizations may be performed, according to the method of Sambrook et al., (supra) using a hybridization solution comprising: 5X SSC, 5X Denhardt's reagent, 1.0% SDS, 100 μg/ml denatured, fragmented salmon sperm DNA, 0.05% sodium pyrophosphate and up to 50% formamide. Hybridization is carried out at 37-42°C for at least six hours. Following hybridization, filters are washed as follows: (1) 5 minutes at room temperature in 2X SSC and 1% SDS; (2) 15 minutes at room temperature in 2X SSC and

0.1% SDS; (3) 30 minutes-1 hour at 37°C in 1X SSC and 1% SDS; (4) 2 hours at 42-65°in 1X SSC and 1% SDS, changing the solution every 30 minutes.

Nucleic acids of the present invention may be maintained as DNA in any convenient cloning vector. In a preferred embodiment, clones are maintained in a plasmid cloning/expression vector, such as pBluescript (Stratagene, La Jolla, CA), which is propagated in a suitable *E. coli* host cell.

MOAT-encoding nucleic acid molecules of the invention include cDNA, genomic DNA, RNA, and fragments thereof which may be single- or double-stranded. Thus, this invention provides oligonucleotides (sense or antisense strands of DNA or RNA) having sequences capable of hybridizing with at least one sequence of a nucleic acid molecule of the present invention, such as selected segments of the cDNA having Sequence I.D. No. 1. Such oligonucleotides are useful as probes for detecting or isolating MOAT genes. Antisense nucleic acid molecules may be targeted to translation initiation sites and/or splice sites to inhibit the translation of the MOAT-encoding nucleic acids of the invention. Such antisense molecules are typically between 15 and 30 nucleotides and length and often span the translational start site of MOAT encoding mRNA molecules.

It will be appreciated by persons skilled in the art that variants of these sequences exist in the human population, and must be taken into account when designing and/or utilizing oligos of the invention. Accordingly, it is within the scope of the present invention to encompass such variants, with respect to the MOAT sequences disclosed herein or the oligos targeted to specific locations on the respective genes or RNA transcripts.

With respect to the inclusion of such variants, the term "natural allelic variants" is used herein to refer to various specific nucleotide sequences and variants thereof that would occur in a human population. The usage of different wobble codons and genetic polymorphisms which give rise to conservative or neutral amino acid substitutions in the encoded protein are examples of such variants. Additionally, the term "substantially complementary" refers to oligo sequences that may not be perfectly matched to a target sequence, but the mismatches do not materially affect the ability of the oligo to hybridize with its target sequence under the conditions described.

B. Proteins

Full-length MOAT-B, MOAT-C, MOAT-D and MOAT-E proteins of the present invention may be prepared in a variety of ways, according to known methods. The proteins may be purified from appropriate sources, e.g., transformed bacterial or animal cultured cells or tissues, by immunoaffinity purification. However, this is not a preferred method due to the low amount of protein likely to be present in a given cell type at any time. The availability of nucleic acid molecules encoding MOAT proteins enables production of the proteins using *in vitro* expression methods known in the art. For example, a cDNA or gene may be cloned into an appropriate *in vitro* transcription vector, such as pSP64 or pSP65 for *in vitro* transcription, followed by cell-free translation in a suitable cell-free translation system, such as wheat germ or rabbit reticulocytes. *In vitro* transcription and translation systems are commercially available, e.g., from Promega Biotech, Madison, Wisconsin or Gibco-BRL,

Gaithersburg, Maryland.

Alternatively, according to a preferred embodiment, larger quantities of MOAT proteins may be produced by expression in a suitable prokaryotic or eukaryotic system. For example, part or all of a DNA molecule, such as a cDNA having Sequence I.D. No. 1, 3, 5 or 7 may be inserted into a plasmid vector adapted for expression in a bacterial cell, such as *E. coli*. Such vectors comprise the regulatory elements necessary for expression of the DNA in the host cell positioned in such a manner as to permit expression of the DNA in the host cell. Such regulatory elements required for expression include promoter sequences, transcription initiation sequences and, optionally, enhancer sequences.

The human MOAT proteins produced by gene expression in a recombinant procaryotic or eukaryotic system may be purified according to methods known in the art. In a preferred embodiment, a commercially available expression/secretion system can be used, whereby the recombinant protein is expressed and thereafter secreted from the host cell, to be easily purified from the surrounding medium. If expression/secretion vectors are not used, an alternative approach involves purifying the recombinant protein by affinity separation, such as by immunological interaction with antibodies that bind specifically to the recombinant protein or nickel columns for isolation of recombinant proteins tagged with 6-8 histidine residues at their N-terminus or C-terminus. Alternative tags may comprise the FLAG epitope or the hemagglutinin epitope. Such methods are commonly used by skilled practitioners.

The human MOAT proteins of the invention, prepared by the aforementioned methods, may be analyzed according to

standard procedures. For example, such proteins may be subjected to amino acid sequence analysis, according to known methods.

The present invention also provides antibodies capable of immunospecifically binding to proteins of the invention. Polyclonal antibodies directed toward human MOAT proteins may be prepared according to standard methods. In a preferred embodiment, monoclonal antibodies are prepared, which react immunospecifically with the various epitopes of the MOAT proteins described herein. Monoclonal antibodies may be prepared according to general methods of Köhler and Milstein, following standard protocols. Polyclonal or monoclonal antibodies that immunospecifically interact with MOAT proteins can be utilized for identifying and purifying such proteins. For example, antibodies may be utilized for affinity separation of proteins with which they immunospecifically interact. Antibodies may also be used to immunoprecipitate proteins from a sample containing a mixture of proteins and other biological molecules. Other uses of anti-MOAT antibodies are described below.

II. Uses of MOAT-Encoding Nucleic Acids, <u>MOAT Proteins and Antibodies Thereto</u>

Cellular transporter molecules have received a great deal of attention as potential targets of chemotherapeutic agents designed to effectively block the export of pharmacological reagents from tumor cells. The MOAT proteins of the invention play a pivotal role in the transport of molecules across the cell membrane.

Additionally, MOAT nucleic acids, proteins and antibodies thereto, according to this invention, may be used as research tools to identify other proteins that are

intimately involved in the transport of molecules into and out of cells. Biochemical elucidation of molecular mechanisms which govern such transport will facilitate the development of novel anti-transport agents that may sensitize tumor cells to conventional chemotherapeutic agents.

A. MOAT-Encoding Nucleic Acids

MOAT-encoding nucleic acids may be used for a variety of purposes in accordance with the present invention. MOAT-encoding DNA, RNA, or fragments thereof may be used as probes to detect the presence of and/or expression of genes encoding MOAT proteins. Methods in which MOAT-encoding nucleic acids may be utilized as probes for such assays include, but are not limited to: (1) *in situ* hybridization; (2) Southern hybridization (3) northern hybridization; and (4) assorted amplification reactions such as polymerase chain reactions (PCR).

The MOAT-encoding nucleic acids of the invention may also be utilized as probes to identify related genes from other animal species. As is well known in the art, hybridization stringencies may be adjusted to allow hybridization of nucleic acid probes with complementary sequences of varying degrees of homology. Thus, MOAT-encoding nucleic acids may be used to advantage to identify and characterize other genes of varying degrees of relation to the MOAT genes of the invention. Such information enables further characterization of transporter molecules which give rise to the chemoresistant phenotype of certain tumors. Additionally, they may be used to identify genes encoding proteins that interact with MOAT proteins (e.g., by the "interaction trap" technique), which should further accelerate

identification of the components involved in the acquisition of drug resistance. The MOAT encoding nucleic acids may also be used to generate primer sets suitable for PCR amplification of target MOAT DNA. Criteria for selecting suitable primers are well known to those of ordinary skill in the art.

Nucleic acid molecules, or fragments thereof, encoding MOAT genes may also be utilized to control the production of MOAT proteins, thereby regulating the amount of protein available to participate in cytotoxic drug efflux. As mentioned above, antisense oligonucleotides corresponding to essential processing sites in MOAT-encoding mRNA molecules may be utilized to inhibit MOAT protein production in targeted cells. Alterations in the physiological amount of MOAT proteins may dramatically affect the ability of these proteins to transport pharmacological reagents out of the cell.

Host cells comprising at least one MOAT encoding DNA molecule are encompassed in the present invention. Host cells contemplated for use in the present invention include but are not limited to bacterial cells, fungal cells, insect cells, mammalian cells, and plant cells. The MOAT encoding DNA molecules may introduced singly into such host cells or in combination to assess the phenotype of cells conferred by such expression. Methods for introducing DNA molecules are also well known to those of ordinary skill in the art. Such methods are set forth in Ausubel et al. eds., Current Protocols in Molecular Biology, John Wiley & Sons, NY, NY 1995, the disclosure of which is incorporated by reference herein.

The availability of MOAT encoding nucleic acids enables the production of strains of laboratory mice carrying part or all of the MOAT genes or mutated

sequences thereof. Such mice may provide an in vivo model for development of novel chemotherapeutic agents. Alternatively, the MOAT nucleic acid sequence information provided herein enables the production of knockout mice in which the endogenous genes encoding MOAT-B, MOAT-C, MOAT-D or MOAT-E have been specifically inactivated. Methods of introducing transgenes in laboratory mice are known to those of skill in the art. Three common methods include: 1. integration of retroviral vectors encoding the foreign gene of interest into an early embryo; 2. injection of DNA into the pronucleus of a newly fertilized egg; and 3. the incorporation of genetically manipulated embryonic stem cells into an early embryo.

The alterations to the MOAT gene envisioned herein include modifications, deletions, and substitutions. Modifications and deletions render the naturally occurring gene nonfunctional, producing a "knock out" animal. Substitutions of the naturally occurring gene for a gene from a second species results in an animal which produces an MOAT gene from the second species. Substitution of the naturally occurring gene for a gene having a mutation results in an animal with a mutated MOAT protein. A transgenic mouse carrying the human MOAT gene is generated by direct replacement of the mouse MOAT gene with the human gene. These transgenic animals are valuable for use in vivo assays for elucidation of other medical disorders associated with cellular activities modulated by MOAT genes. A transgenic animal carrying a "knock out" of a MOAT encoding nucleic acid is useful for the establishment of a nonhuman model for chemotherapy resistance involving MOAT regulation.

As a means to define the role that MOAT plays in mammalian systems, mice can be generated that cannot make

MOAT proteins because of a targeted mutational disruption of a MOAT gene.

The term "animal" is used herein to include all vertebrate animals, except humans. It also includes an individual animal in all stages of development, including embryonic and fetal stages. A "transgenic animal" is any animal containing one or more cells bearing genetic information altered or received, directly or indirectly, by deliberate genetic manipulation at the subcellular level, such as by targeted recombination or microinjection or infection with recombinant virus. The term "transgenic animal" is not meant to encompass classical cross-breeding or in vitro fertilization, but rather is meant to encompass animals in which one or more cells are altered by or receive a recombinant DNA molecule. This molecule may be specifically targeted to defined genetic locus, be randomly integrated within a chromosome, or it may be extrachromosomally replicating DNA. The term "germ cell line transgenic animal" refers to a transgenic animal in which the genetic alteration or genetic information was introduced into a germ line cell, thereby conferring the ability to transfer the genetic information to offspring. If such offspring in fact, possess some or all of that alteration or genetic information, then they, too, are transgenic animals.

The alteration or genetic information may be foreign to the species of animal to which the recipient belongs, or foreign only to the particular individual recipient, or may be genetic information already possessed by the recipient. In the last case, the altered or introduced gene may be expressed differently than the native gene.

The altered MOAT gene generally should not fully encode the same MOAT protein native to the host animal and

its expression product should be altered to a minor or great degree, or absent altogether. However, it is conceivable that a more modestly modified MOAT gene will fall within the compass of the present invention if it is a specific alteration.

The DNA used for altering a target gene may be obtained by a wide variety of techniques that include, but are not limited to, isolation from genomic sources, preparation of cDNAs from isolated mRNA templates, direct synthesis, or a combination thereof.

A preferred type of target cell for transgene introduction is the embryonal stem cell (ES). ES cells may be obtained from pre-implantation embryos cultured in vitro. Transgenes can be efficiently introduced into the ES cells by standard techniques such as DNA transfection or by retrovirus-mediated transduction. The resultant transformed ES cells can thereafter be combined with blastocysts from a non-human animal. The introduced ES cells thereafter colonize the embryo and contribute to the germ line of the resulting chimeric animal.

One approach to the problem of determining the contributions of individual genes and their expression products is to use isolated MOAT genes to selectively inactivate the wild-type gene in totipotent ES cells (such as those described above) and then generate transgenic mice. The use of gene-targeted ES cells in the generation of gene-targeted transgenic mice is known in the art.

Techniques are available to inactivate or alter any genetic region to a mutation desired by using targeted homologous recombination to insert specific changes into chromosomal alleles. However, in comparison with homologous extrachromosomal recombination, which occurs at a frequency approaching 100%, homologous plasmid-

chromosome recombination was originally reported to only be detected at frequencies between 10^{-6} and 10^{-3}. Nonhomologous plasmid-chromosome interactions are more frequent occurring at levels 10^5-fold to 10^2-fold greater than comparable homologous insertion.

To overcome this low proportion of targeted recombination in murine ES cells, various strategies have been developed to detect or select rare homologous recombinants. One approach for detecting homologous alteration events uses the polymerase chain reaction (PCR) to screen pools of transformant cells for homologous insertion, followed by screening of individual clones. Alternatively, a positive genetic selection approach has been developed in which a marker gene is constructed which will only be active if homologous insertion occurs, allowing these recombinants to be selected directly. One of the most powerful approaches developed for selecting homologous recombinants is the positive-negative selection (PNS) method developed for genes for which no direct selection of the alteration exists. The PNS method is more efficient for targeting genes which are not expressed at high levels because the marker gene has its own promoter. Non-homologous recombinants are selected against by using the Herpes Simplex virus thymidine kinase (HSV-TK) gene and selecting against its nonhomologous insertion with effective herpes drugs such as gancyclovir (GANC) or (1-(2-deoxy-2-fluoro-B-D arabinofluranosyl)-5-iodouracil, (FIAU). By this counter selection, the number of homologous recombinants in the surviving transformants can be increased.

As used herein, a "targeted gene" or "knock-out" is a DNA sequence introduced into the germline or a non-human animal by way of human intervention, including but not

limited to, the methods described herein. The targeted genes of the invention include DNA sequences which are designed to specifically alter cognate endogenous alleles.

Methods of use for the transgenic mice of the invention are also provided herein. Knockout mice of the invention can be injected with tumor cells or treated with carcinogens to generate carcinomas. Such mice provide a biological system for assessing chemotherapy resistance as modulated by a MOAT gene of the invention. Accordingly, therapeutic agents which inhibit the action of these transporters and thereby prevent efflux of beneficial chemotherapeutic agents from tumor cells may be screened in studies using MOAT knock out mice.

As described above, MOAT-encoding nucleic acids are also used to advantage to produce large quantities of substantially pure MOAT proteins, or selected portions thereof.

B. MOAT Proteins and Antibodies

Purified full length MOAT proteins, or fragments thereof, may be used to produce polyclonal or monoclonal antibodies which also may serve as sensitive detection reagents for the presence and accumulation of MOAT proteins (or complexes containing MOAT proteins) in mammalian cells. Recombinant techniques enable expression of fusion proteins containing part or all of MOAT proteins. The full length proteins or fragments of the proteins may be used to advantage to generate an array of monoclonal antibodies specific for various epitopes of MOAT proteins, thereby providing even greater sensitivity for detection of MOAT proteins in cells.

Polyclonal or monoclonal antibodies immunologically specific for MOAT proteins may be used in

a variety of assays designed to detect and quantitate the proteins. Such assays include, but are not limited to: (1) flow cytometric analysis; (2) immunochemical localization of MOAT proteins in tumor cells; and (3) immunoblot analysis (e.g., dot blot, Western blot) of extracts from various cells. Additionally, as described above, anti-MOAT antibodies can be used for purification of MOAT proteins and any associated subunits (e.g., affinity column purification, immunoprecipitation).

From the foregoing discussion, it can be seen that MOAT-encoding nucleic acids, MOAT expressing vectors, MOAT proteins and anti-MOAT antibodies of the invention can be used to detect MOAT gene expression and alter MOAT protein accumulation for purposes of assessing the genetic and protein interactions involved in the development of drug resistance in tumor cells.

C. **Methods and Kits Employing the <u>Compositions of the Present Invention</u>**

From the foregoing discussion, it can be seen that MOAT-encoding nucleic acids, MOAT-expressing vectors, MOAT proteins and anti-MOAT antibodies of the invention can be used to detect MOAT gene expression and alter MOAT protein accumulation for purposes of assessing the genetic and protein interactions giving rise to chemotherapy resistance in tumor cells.

Exemplary approaches for detecting MOAT nucleic acid or polypeptides/proteins include:

a) comparing the sequence of nucleic acid in the sample with the MOAT nucleic acid sequence to determine whether the sample from the patient contains mutations;or

b) determining the presence, in a sample from a patient, of the polypeptide encoded by the MOAT gene and,

if present, determining whether the polypeptide is full length, and/or is mutated, and/or is expressed at the normal level; or

c) using DNA restriction mapping to compare the restriction pattern produced when a restriction enzyme cuts a sample of nucleic acid from the patient with the restriction pattern obtained from normal MOAT gene or from known mutations thereof; or,

d) using a specific binding member capable of binding to a MOAT nucleic acid sequence (either normal sequence or known mutated sequence), the specific binding member comprising nucleic acid hybridizable with the MOAT sequence, or substances comprising an antibody domain with specificity for a native or mutated MOAT nucleic acid sequence or the polypeptide encoded by it, the specific binding member being labelled so that binding of the specific binding member to its binding partner is detectable; or,

e) using PCR involving one or more primers based on normal or mutated MOAT gene sequence to screen for normal or mutant MOAT gene in a sample from a patient.

A "specific binding pair" comprises a specific binding member (sbm) and a binding partner (bp) which have a particular specificity for each other and which in normal conditions bind to each other in preference to other molecules. Examples of specific binding pairs are antigens and antibodies, ligands and receptors and complementary nucleotide sequences. The skilled person is aware of many other examples and they do not need to be listed here. Further, the term "specific binding pair" is also applicable where either or both of the specific binding member and the binding partner comprise a part of a large molecule. In embodiments in which the specific

binding pair are nucleic acid sequences, they will be of a length to hybridize to each other under conditions of the assay, preferably greater than 10 nucleotides long, more preferably greater than 15 or 20 nucleotides long.

In most embodiments for screening for alleles giving rise to chemotherapy resistance, the MOAT nucleic acid in biological sample will initially be amplified, e.g. using PCR, to increase the amount of the analyte as compared to other sequences present in the sample. This allows the target sequences to be detected with a high degree of sensitivity if they are present in the sample. This initial step may be avoided by using highly sensitive array techniques that are becoming increasingly important in the art.

The identification of the MOAT gene and its association with a particular chemotherapy resistance paves the way for aspects of the present invention to provide the use of materials and methods, such as are disclosed and discussed above, for establishing the presence or absence in a test sample of a variant form of the gene, in particular an allele or variant specifically associated with chemotherapy resistance. This may be done to assess the propensity of the tumor to exhibit chemotherapy resistance.

In still further embodiments, the present invention concerns immunodetection methods for binding, purifying, removing, quantifying or otherwise generally detecting biological components. The encoded proteins or peptides of the present invention may be employed to detect antibodies having reactivity therewith, or, alternatively, antibodies prepared in accordance with the present invention, may be employed to detect the encoded proteins or peptides. The steps of various useful immunodetection methods have been

described in the scientific literature, such as, e.g., Nakamura et al. (1987).

In general, the immunobinding methods include obtaining a sample suspected of containing a protein, peptide or antibody, and contacting the sample with an antibody or protein or peptide in accordance with the present invention, as the case may be, under conditions effective to allow the formation of immunocomplexes.

The immunobinding methods include methods for detecting or quantifying the amount of a reactive component in a sample, which methods require the detection or quantitation of any immune complexes formed during the binding process. Here, one would obtain a sample suspected of containing a MOAT gene encoded protein, peptide or a corresponding antibody, and contact the sample with an antibody or encoded protein or peptide, as the case may be, and then detect or quantify the amount of immune complexes formed under the specific conditions.

In terms of antigen detection, the biological sample analyzed may be any sample that is suspected of containing the MOAT antigen, such as a tumor tissue section or specimen, a homogenized tissue extract, an isolated cell, a cell membrane preparation, separated or purified forms of any of the above protein-containing compositions.

Contacting the chosen biological sample with the protein, peptide or antibody under conditions effective and for a period of time sufficient to allow the formation of immune complexes (primary immune complexes) is generally a matter of simply adding the composition to the sample and incubating the mixture for a period of time long enough for the antibodies to form immune complexes with, i.e., to bind to, any antigens present. After this time, the sample-antibody composition, such as a tissue

section, ELISA plate, dot blot or Western blot, will generally be washed to remove any non-specifically bound antibody species, allowing only those antibodies specifically bound within the primary immune complexes to be detected.

In general, the detection of immunocomplex formation is well known in the art and may be achieved through the application of numerous approaches. These methods are generally based upon the detection of a label or marker, such as any radioactive, fluorescent, biological or enzymatic tags or labels of standard use in the art. U.S. Patents concerning the use of such labels include U.S. Pat. Nos. 3,817,837; 3,850,752; 3,939,350; 3,996,345; 4,277,437; 4,275,149 and 4,366,241, each incorporated herein by reference. Of course, one may find additional advantages through the use of a secondary binding ligand such as a second antibody or a biotin/avidin ligand binding arrangement, as is known in the art.

In one broad aspect, the present invention encompasses kits for use in detecting expression of MOAT encoding nucleic acids in biological samples, including biopsy samples. Such a kit may comprise one or more pairs of primers for amplifying nucleic acids corresponding to the MOAT gene. The kit may further comprise samples of total mRNA derived from tissues expressing at least one or a subset of the MOAT genes of the invention, to be used as controls. The kit may also comprise buffers, nucleotide bases, and other compositions to be used in hybridization and/or amplification reactions. Each solution or composition may be contained in a vial or bottle and all vials held in close confinement in a box for commercial sale. In a further embodiment, the invention encompasses a kit for use in detecting MOAT proteins in chemotherapy

resistant cancer cells comprising antibodies specific for MOAT proteins encoded by the MOAT nucleic acids of the present invention.

Another aspect of the present invention comprises screening methods employing host cells expressing one or more MOAT genes of the invention. An advantage of having discovered the complete coding sequenced of MOAT B-E is that cell lines that overexpress MOATB C D or E can be generated using standard transfection protocols. Cells that overexpress the complete cDNA will also harbor the complete proteins, a feature that is essential for biological activity of proteins. The overexpressing cell lines will be useful in several ways: 1)The drug sensitivity of overexpressing cell lines can be tested with a variety of known anticancer agents in order to determine the spectrum of anticancer agents for which the transporter confers resistance; 2)The drug sensitivity of overexpressing cell lines can be used to determine whether newly discovered anticancer agents are transported out of the cell by one of the discovered transporters; 3)Overexpressing cell lines can be used to identify potential inhibitors that reduce the activity of the transporters. Such inhibitors are of great clinical interest in that they may enhance the activity of known anticancer agents, thereby increasing their effectiveness. Reduced activity will be detected by restoration of anticancer drug sensitivity, or by reduction of transporter mediated cellular efflux of anticancer agents. In vitro biochemical studies designed to identify reduced transporter activity in the presence of potential inhibitors can also be performed using membranes prepared from overexpessing cell lines; and 4)Overexpressing cell lines can also be used to

determine whether pharmaceutical agents that are not anticancer agents are transported out of the cell by the transporters.

The following protocols are provided to facilitate the practice of the present invention.

Isolation of MOAT-B cDNA

Forward {CT(A/G/T) GT(A/G/T) GC(A/G/T) GT(A/G/T) GT(A/G/T) GG(A/G/C/T)}(SEQ ID NO:9) and reverse {(G/A)CT (A/G/C/T)A(A/G/C) (A/G/C/T)GC (A/G/C/T)(G/C)(T/A) (A/G/C/T)A(A/G) (A/G/C/T)GG (A/G/C/T)TC (A/G)TC}(SEQ ID NO:16) degenerate oligonucleotide primers were designed based upon the first nucleotide binding folds of human MRP, CFTR, and MDR1. Bacteriophage DNA isolated from a C200 cDNA library prepared in the λpCEV27 phagemid vector (17) was used as template in PCR reactions containing 250 ng cDNA, 5 μM primers, 50 mM KCl, 10 mM Tris-HCl, pH 8.3, 3 mM $MgCl_2$, .05% gelatin, 0.2 mM dNTP and Taq polymerase (Perkin Elmer Cetus). Five cycles of PCR were performed as follows: 94°C for 1 minute, 40°C for 2 minutes, 72°C for 3 minutes. Twenty five cycles were then performed as follows: 94°C for 1 minute, 55°C for 1 minute, and 72°C for 1 minute. The resulting reaction products were used as template in a second round of PCR, as described above, with nested forward {CGGGATCC AG(A/G) GA(A/G) AA(C/T) AT(A/C/T) CT(A/G/C/T) TTT GG(A/G/C/T)}(SEQ ID NO:17) and reverse {CGGAATTC (A/G/T/C)TC (A/G)TC (A/C/T)AG (A/G/C/T)AG (A/G)TA (A/T/G)AT (A/G)TC}(SEQ ID NO:18) degenerate oligonucleotide primers. PCR reaction products were isolated from an agarose gel and subcloned into the BamHI and EcoRI sites of pBluescript (Stratagene). Nucleotide sequence analysis

was performed on plasmid DNA prepared from ampicillin resistant transformants. Additional cDNA clones were isolated from C200 (ovary) and B5 (breast) cDNA libraries by plaque hybridization using the PCR product as the initial radiolabeled probe.

RNA Blot Analysis

Blots containing polyA$^+$ RNA isolated from human tissues (Clontech) were prehybridized at 45°C for 8 hours in 50% formamide, 4X SSC, 4X Denhardt's solution, 0.04 M sodium phosphate monobasic, pH 6.5, 0.8% (w/v) glycine, 0.1 mg/ml sheared denatured salmon sperm DNA. Hybridization was performed at 45°C with ^{32}P-labeled MOAT-B or GAPDH probes in a solution containing 50% formamide, 3X SSC, 0.04 M sodium phosphate pH 6.5, 10% dextran sulfate, 0.1 mg/ml sheared denatured salmon sperm DNA. Blots were washed 2 times for 15 min at 65°C in 2X SSC, 5 mM Tris-HCl pH7.4, 0.5% SDS, 2.5 mM EDTA, 0.1% sodium pyrophosphate pH 8.0, and subsequently washed 2 times for 15 min in 0.1X SSC. Blots were then subjected to autoradiography.

Chromosomal localization

Preparation of metaphase spreads from phytohemagglutinin-stimulated lymphocytes of a healthy female donor, and fluorescence *in situ* hybridization and detection of immunofluorescence were carried out as previously described (18). A 2.2-kb cDNA clone of MOAT-B inserted in pBluescript was biotinylated by nick translation in a reaction containing 1 μg DNA, 20 μM each of dATP, dCTP and dGTP, 1 μM dTTP, 25 mM Tris-HCl, pH 7.5, 5 mM $MgCl_2$, 10 mM ß-mercaptoethanol, 10μM biotin-16-dUTP (Boehringer Mannheim), 2 units DNA polymerase 1/DNase 1 (GIBCO, BRL) and water to a total volume of 50 μl. The

probe was denatured and hybridized to metaphase spreads overnight at 37°C. Hybridization sites were detected with fluorescein-labeled avidin (Oncor) and amplified by addition of anti-avidin antibody (Oncor) and a second layer of fluorescein-labeled avidin. The chromosome preparations were counterstained with DAPI and observed with a Zeiss Axiophot epifluorescence microscope equipped with a cooled charge coupled device camera (Photometrics, Tucson AZ) operated by a Macintosh computer work station. Digitized images of DAPI staining and fluorescein signals were captured, pseudo-colored and merged using Oncor Image version 1.6 software.

Isolation of MOAT-C and MOAT-D cDNA

MOAT-C and MOAT-D cDNA clones were isolated by plaque hybridization from bacteriophage cDNA libraries using the I.M.A.G.E. clones as the initial probes (ATCC).

RNA blot analysis

Blots containing polyA$^+$ RNA isolated from human tissues (Clontech) were purchased from Clontech, and hybridized with radiolabeled MOAT-C, MOAT-D or actin probes according to the manufacturer's directions.

Chromosomal localization

Preparation of metaphase spreads from phytohemagglutinin-stimulated lymphocytes of a healthy female donor, and fluorescence *in situ* hybridization and detection of immunofluorescence were carried out as previously described (18). A MOAT-C probe inserted in pBluescript, or MOAT-D probe inserted in pBluescript, was biotinylated by nick translation in a reaction containing 1 μg DNA, 20 μM each of dATP, dCTP and dGTP, 1 μM dTTP, 25

mM Tris-HCl, pH 7.5, 5 mM $MgCl_2$, 10 mM ß-mercaptoethanol, 10μM biotin-16-dUTP (Boehringer Mannheim), 2 units DNA polymerase 1/DNase 1 (GIBCO, BRL) and water to a total volume of 50 μl. The probe was denatured and hybridized to metaphase spreads overnight at 37°C. Hybridization sites were detected with fluorescein-labeled avidin (Oncor) and amplified by addition of anti-avidin antibody (Oncor) and a second layer of fluorescein-labeled avidin. The chromosome preparations were counterstained with DAPI and observed with a Zeiss Axiophot epifluorescence microscope equipped with a cooled charge coupled device camera (Photometrics, Tucson AZ) operated by a Macintosh computer work station. Digitized images of DAPI staining and fluorescein signals were captured, pseudo-colored and merged using Oncor Image version 1.6 software.

The following examples are provided to illustrate various embodiments of the invention. They are not intended to limit the invention in any way.

EXAMPLE I

Isolation of MOAT-B cDNA.

A degenerate PCR approach was used to isolate MRP-related transporters. Degenerate oligonucleotide primers were prepared based upon the N-terminal nucleotide binding folds of MRP and other eukaryotic transporters, and used in conjunction with DNA prepared from an ovarian cancer cell line bacteriophage library. Nucleotide sequence analysis of one of the resulting PCR products indicated that it encoded a segment of a novel nucleotide binding fold that was most closely related to MRP and cMOAT. Overlapping cDNA clones were isolated from ovarian and breast bacteriophage libraries by plaque hybridization using the PCR product as the initial probe. A total of

5.9 kB of cDNA was isolated. Nucleotide sequence analysis revealed two classes of cDNA clones that were about equally represented among isolates from each of the two bacteriophage libraries. The first class contained an open reading frame of 3975 bp that was bordered by in frame stop codons located at positions -76 and -42 (relative to the putative initiation codon) and 3976, and encoding a predicted protein of 1325 amino acids, which is designated MOAT-B. The open reading frame was followed by approximately 2 kB of 3' untranslated sequences. The most upstream ATG in the open reading frame was located in the sequence context $^{-4}$CAAG**ATG**C^{+4}. The A at position -3 of the putative translation initiation codon was in agreement with the major feature of the Kozak consensus sequence, but the C at position +4 was divergent from the more usual G. The second class of cDNA clones was identical to the first with the exception of a single nucleotide. These clones harbored an additional T following nucleotide 3872 of the first class of clones, close to the C-terminus of the predicted protein. This additional nucleotide resulted in a frame shift such that the predicted protein of the second class of cDNA clones was 22 residues shorter than that of the first class of cDNA clones, and in which the C-terminal 34 residues of the latter reading frame were replaced by 12 distinct residues. See brief description of Figure 1.

Analysis of the MOAT-B Predicted Structure.

Comparison of the MOAT-B predicted protein with complete coding sequences in protein data bases using the BLAST program indicated that it shared significant similarity with several eukaryotic ABC transporters. Table I.

Table I. Comparison of peptide domains of MOAT-B with those of other eukaryotic ABC transporters

MOAT-B Domain (peptide)	TM1 (88-376)	NBF1 (428-576)	linker region (577-705)	TM2 (706-992)	NBF2 (1058-1216)	C-terminus (1217-1325)	overall identity
	percent identity						
MRP human	28.6	55.6	27.9	33.3	61.6	51.6	39.2
YCF1 yeast	27	56	27.9	34	57.2	48.5	38.9
MOAT human	33.2	53.3	32.8	31.4	55.3	44.9	38
CFTR Human	30.5	48	27.9	37.7	44	21	36.3
SUR rat	28.1	41.3	28.2	30	52.8	42.8	32.9
MDR1 human	17.6	39.2	21.1	17.3	32.2	40.3	23.3

[B] The indicated domains are, TM1: segment containing the transmembrane spanning domain N-terminal to NBF1; NBF1 and NBF2: nucleotide binding folds 1 and 2; Linker region: segment located between NBF1 and TM2;TM2: segment containing the transmembrane spanning domain located between the two NBFs; C-terminus: segment between NBF2 and the C-terminus of the proteins. Sequence alignments were generated using the PILEUP program of the GCC package. Percent amino acid identity with MOAT-B domains are shown.

Typical features of eukaryotic ABC transporters were present in the predicted MOAT-B protein. See Figure 1. Overall the protein was composed of a tandem repeat of a nucleotide binding fold appended C-terminal to a hydrophobic domain that contained several potential transmembrane spanning helices. Conserved Walker A and B ATP binding sites were present in each of the nucleotide binding folds. See Figure 2A. In addition, a conserved C motif, the signature sequence of ABC transporters, was present in each nucleotide binding fold. Analysis of potential transmembrane motifs using the TMAP program (19) and an input sequence alignment of MOAT-B and MOAT-C, a transporter highly related to MOAT-B[4], predicted 12 transmembrane helices with 6 transmembrane segments in

each of the two hydrophobic domains. This 6 + 6 configuration of predicted transmembrane helices is in agreement with topological models proposed for MRP and other ABC transporters (20, 21), and is shown in Figure 1. However, alternative predictions of transmembrane segments were obtained using different program parameters or input sequence alignments. For example, when the TMAP program was used with an input sequence alignment consisting of human MRP, rat cMOAT, rat sulfonyl urea receptor (SUR), human cystic fibrosis conductance regulator (CFTR) and human P-glycoprotein, a 6 + 5 configuration was predicted. The only substantial difference between the latter prediction and the structure shown in Figure 1 is that transmembrane segments 9 (829-853) and 10 (855-878) were replaced by a single predicted transmembrane segment spanning amino acids 847 - 875.

Among ABC transporters, the degree of similarity of the nucleotide binding folds is considered to be the best indicator of functional conservation. Comparison of the nucleotide binding folds of MOAT-B with other eukaryotic ABC transporters indicated that it was most closely related to MRP, the yeast cadmium resistance protein (YCF1) and cMOAT (Table I), three transporters that have organic anions as substrates. The MOAT-B NBF1 was 55.6, 56.0 and 53.3 percent identical, and the MOAT-B NBF2 was 61.6, 57.2 and 55.3 percent identical to the first and second nucleotide binding folds of human MRP, YCF1 and human cMOAT, respectively. Aside from the latter transporters, the MOAT-B nucleotide binding folds were most closely related to those of CFTR and SUR. The MOAT-B nucleotide binding folds shared significantly less similarity with those of MDR1. Alignment of the MOAT-B nucleotide binding folds with those of other eukaryotic

transporters is shown in Figure 2A. Analysis of the overall amino acid identity of MOAT-B with other ABC transporters also indicated that it was most closely related to MRP, YCF1 and cMOAT (Table I). Overall MOAT-B was 39.2, 38.9 and 38 percent identical to these transporters, respectively. Figure 2B shows a comparison of the hydropathy profiles of MOAT-B with those of other eukaryotic transporters. This comparison reveals that MOAT-B (1325 amino acids) is approximately 200 amino acids smaller than MRP (1531 residues), cMOAT (1545 residues) and YCF1 (1515 residues), and that this size difference is largely accounted for by the absence in MOAT-B of an amino terminal hydrophobic extension that is present in MRP, cMOAT and YCF1 (22). This N-terminal hydrophobic segment is predicted to harbor several transmembrane spanning segments, and is also present in SUR.

Expression Pattern of MOAT-B in Human Tissues.

To gain insight into the possible function of MOAT-B, its expression pattern in a variety of human tissues was examined by RNA blot analysis. As shown in Figure 3, a MOAT-B transcript of approximately 6 kB was readily detected. The isolation of 5.9 kB of MOAT-B cDNA was consistent with this size. MOAT-B expression was detected in each of the 16 tissues analyzed. Transcript levels were highest in prostate and lowest in liver and peripheral blood leukocytes, for which prolonged exposure of film were required to detect expression. Intermediate levels of expression were observed in other tissues.

Chromosomal Localization of the *MOAT-B* Gene.

The *MOAT-B* chromosomal localization was determined by fluorescence *in situ* hybridization. As shown in Figure 4, hybridization of the MOAT-B probe to metaphase spreads revealed specific labeling at human chromosome band 13q32.

Fluorescent signals were detected on chromosome 13 in each of 19 metaphase spreads scored. Of 135 signals observed, 62 (46%) were on 13q. Among these signals, 61 localized at 13q32, near the boundary between 13q31 and 13q32. Paired (on sister chromatids) signals were only seen at band 13q32. In several metaphases, signals on a single chromatid were observed at chromosome bands 6p21 or 4q21, suggesting hybridization to distantly related sequences.

EXAMPLE II

Isolation of MOAT-C and MOAT-D cDNA.

Isolation of the MOAT-B_4 transporter as described above suggested the possibility that there were other MRP/cMOAT-related transporters. A blast search (36) of the nonredundent expressed sequence tag data base using MRP and related yeast transporters revealed two clones with significant similarity to MRP and cMOAT. The first of these sequences (I.M.A.G.E. consortium clone 113196) was 1.2 kb in length, 800 bp of which encoded an MRP-related peptide. A segment of this clone was used as a probe to screen ovarian and hematopoietic bacteriophage libraries. Analysis of these cDNA clones indicated that they contained approximately 2 kb of additional coding sequence not present in clone 113196. An additional 1655 bp of 5' sequence was obtained by several rounds of RACE using the bacteriophage DNA prepared from the ovarian cDNA library as template. The continuity of the sequences obtained by RACE with the cDNA clones isolated from bacteriophage libraries was confirmed by nucleotide sequence analysis of a 2 kb product obtained by RT/PCR using an upstream oligonucleotide primer located at the 5' end of the RACE sequence and a downstream primer located at the 5' end of the cDNA obtained by plaque

hybridization. A total of approximately 5.9 kb of cDNA sequences were isolated. Nucleotide sequence analysis revealed an open reading frame of 4311 bp that was preceded by an in frame stop codon located at positions -93 (relative to the putative initiation codon), and encoding a predicted protein of 1437 amino acids, which is designated MOAT-C herein. The open reading frame was followed by approximately 1.4 kB of 3' untranslated sequences in which a polyadenylation sequence (AAUAAA) was located 20 bp upstream of the poly(A) tail. The most upstream ATG in the open reading frame was located in the sequence context $^{-4}$GAAG**ATG**A^{+4}. The A at position -3 of the putative translation initiation codon was in agreement with the major feature of the Kozak consensus sequence, but the A at position +4 was divergent from the more usual G (37). The second sequence identified in our data base search (I.M.A.G.E. consortium clone 208097) was 1.2 kb in length, of which 588 bp encoded an MRP-related peptide. A segment of this clone was used as a probe to screen liver and monocyte bacteriophage cDNA libraries, and 5' cDNA segments of the isolated cDNA clones were used in a subsequent round of screening. Together approximately 5.2 kb of cDNA sequence were isolated. Nucleotide sequence analysis revealed an open reading frame of 4570 bp, which is designated MOAT-D herein. The open reading frame was followed by approximately 0.6 kb of 3' untranslated sequences in which a polyadenylation sequence (AAUAAA) was located 12 bp upstream of the poly(A) tail. An upstream in frame stop codon was not present in the MOAT-D cDNA clones, and attempts to obtain additional upstream sequences by RACE using as template cDNA prepared from sources in which MOAT-D is abundant were not successful. The most upstream ATG in the open reading frame

(nucleotide position 5-7), located in the sequence context $^{-4}$ATGG**ATG**G^{+4}, was therefore designated as the translational initiation site. The G at position +4, was in good agreement with the Kozak consensus sequence, but the T at -3 was divergent from the more usual A (37). Although an upstream in frame stop codon was not identified in the MOAT-D cDNA clones, the size of the encoded protein was within one amino acid of the size of the transporter with which it shares the highest degree of identity (MRP), suggesting that the complete MOAT-D open reading frame was present in the isolated cDNA clones.

Analysis of the MOAT-C and MOAT-D Predicted Proteins.

Comparison of the MOAT-C and MOAT-D predicted proteins with complete coding sequences in protein data bases using the BLAST program indicated that they shared significant similarity with several eukaryotic ABC transporters. Typical features of eukaryotic ABC transporters were present in the predicted proteins. See Figure 5. Overall the proteins were composed of hydrophobic domains containing potential transmembrane spanning helices and two nucleotide binding folds. Conserved Walker A and B ATP binding sites, as well as a conserved C motif, the signature sequence of ABC transporters, was present in the nucleotide binding folds. Computer assisted analysis of potential transmembrane helices of MOAT-C using the TMAP program (19) predicted 12 transmembrane helices with 6 transmembrane spanning helices in each of two membrane spanning domains. This 6 + 6 (TM1-TM6 and TM7-TM12) configuration of predicted transmembrane helices is in agreement with topological models proposed for several other ABC transporters (20, 21), and is shown in Figure 5. However, alternative

predictions of transmembrane segments were obtained using different program parameters or input sequence alignments. Comparison of the hydropathy profiles of MOAT-C with other MRP/cMOAT-related transporters (Fig. 6B) indicates that its structure is similar to that of MOAT-B, which also has two membrane spanning domains.

In contrast to MOAT-C, hydrophobicity analysis of MOAT-D indicated that it has three membrane spanning domains. Similar to MRP, cMOAT and the yeast cadmium resistance factor 1 (YCF1), MOAT-D has an additional N-terminal hydrophobic domain that is not present in MOAT-B or MOAT-C (Figs. 5 and 6). A 5+6+6 configuration of transmembrane spanning helices has been proposed for MRP (38), in which the N-terminal extension harbors 5 transmembrane spanning helices, and 6 transmembrane helices are present in the second and third membrane spanning domain. An alignment of the MOAT-D predicted protein with MRP using the GAP program indicated that proposed MRP transmembrane spanning helices were conserved in MOAT-D. This 5+6+6 model for MOAT-D is shown in Fig. 5. Another configuration of transmembrane spanning helices (5+6+4) was predicted using computer assisted analysis. MRP has been reported to have two N-linked glycosylation sites in its N-terminus (Asn-19 and Asn-23) and another site located between the first and second transmembrane spanning helix of its third membrane spanning domain (Asn-1006). The alignment of MOAT-D with MRP indicated that an N-terminal (Asn-21) and a distal N-glycosylation sites (Asn-1008/1009) were conserved in analogous positions in MOAT-D. Only the distal N-glycosylation site of MRP is conserved in MOAT-C (Asn890) (Fig. 5) and MOAT-B[4] (Asn746/754).

Among ABC transporters, the degree of similarity of

the nucleotide binding folds is considered to be the best indicator of functional conservation. Comparison of the nucleotide binding folds of MOAT-C and MOAT-D with other eukaryotic ABC transporters indicated that they were most closely related to those of human MRP, human cMOAT and yeast YCF1, three transporters that have organic anions as substrates. As shown in Table 2, among the human transporters, the MOAT-C NBF1 was about equally related to MOAT-D, MRP and cMOAT (55-61% identity), and less similar to MOAT-B (49% identity).

Table II. Amino acid identity: nucleotide binding folds 1 and 2 of MRP/cMOAT sub-family members.

	MOAT-C	MOAT-D	MOAT-B	MRP	cMOAT	YCFI
			%IDENTIFY (BNF1/NBF20)			
MOAT-C	-----	57.3/58.9	49.3/59.1	60.0/59.4	61.3/60.6	55.3/58/8
MOAT-D	57.3/58/9	-----	55.3/54.1	70.173.8	67.3/70.0	52.7/61.3
MOAT-B	49.3/59.1	55.3/54.1	-----	57.3/61/6	53.3/55.3	56.0/57.2
MRP	60.0/59.4	70.7/73.7	57.3/61.6	-----	66.0/73.1	53.3/63.8
cMOAT	61/3/60.6	67.3/70.0	53.3/55.3	66.0/73.1	-----	50.7/61/3
YCF1	55.3/58.8	52.7/61.3	56.0/57.2	53.3/63.8	50.7/61.3	-----

The MOAT-C NBF2 shared about equal amino acid identity with the five other transporters in this group (59-61% identity). Overall, the MOAT-C protein was about equally related to the other five transporters in this group, with 33.1-36.5% identity. Aside from these

transporters, MOAT-C is most closely related to CFTR, with which its NBFs shared 44%/42 % identity, and SUR, with which its NBFs shared 49%/51% identity.

The MOAT-D NBFs were clearly most closely related to those of MRP and cMOAT, with which they shared considerable amino acid identity (67.3-73.8%). See Table III. Of the latter two transporters, the MOAT-D NBFs were slightly more related to those of MRP. In contrast, the MOAT-D NBFs shared only 55.3-58.9% identity with those of MOAT-C and MOAT-B. Overall, MOAT-D was again most closely related to MRP (57.3%) and cMOAT (46.9%), but significantly more related to MRP. Consistent with the analysis of NBFs, MOAT-D was much less related to MOAT-C and MOAT-B, with which it shared only 33.1% and 35.3% identity, respectively. Alignment of the MOAT-C and MOAT-D nucleotide binding folds with those of other eukaryotic transporters is shown in Fig. 6.

Table III. Overall amino acid identifying among MRP/cMOAT sub-family members

	MOAT-C	MOAT-D	MOAT-B	MRP	cMOAT	YCF1
			%identity			
MOAT-C	----	33.1	36.5	35.8	36.2	33.6
MOAT-D	33.1	----	35.3	57.3	46.9	38.1
MOAT-B	36.4	35.3	----	39.4	36.8	38.8
MRP	35.8	57.3	39.4	----	48.4	46.4
cMOAT	36.3	46.9	36.8	48.8	----	38.8
YCF1	33.6	38.1	38.8	40.4	38.8	----

Expression Pattern of MOAT-C and MOAT-D in Human Tissues.

To gain insight into the possible functions of MOAT-C and MOAT-D, their expression patterns in a variety of human tissues was examined by RNA blot analysis. As

shown in Fig. 7 (upper panels), a MOAT-C transcript of approximately 6.6 kB was readily detected in several tissues. MOAT-C transcript levels were highest in skeletal muscle, with intermediate levels in kidney, testes, heart and brain. Low levels were detected in most other tissues, including spleen, thymus, prostate, ovary, and placenta. Prolonged exposures were required for detection in lung and liver. MOAT-D was expressed as an approximately 6 kb transcript (middle panels). Compared to MOAT-C, the MOAT-D expression pattern was more restricted. MOAT-D was highly expressed in colon and pancreas, with lower levels in liver and kidney. Low levels were detected in small intestine, placenta and prostate. Prolonged exposures were required to detect MOAT- D in testes, thymus, spleen and lung.

Chromosomal localization of the *MOAT-C* and *MOAT-D* genes.

The *MOAT-C and MOAT-D* chromosomal localizations were determined by fluorescence *in situ* hybridization. As shown in Figure 8, hybridization of the MOAT-C probe to metaphase spreads revealed specific labeling at human chromosome band 3q27. Fluorescent signals were detected on chromosome 3q in each of 22 metaphase spreads scored. Of 75 signals observed, 43 (57%) were on 3q. Paired (on sister chromatids) signals were only seen at band 3q27. Hybridization of the MOAT-D probe revealed specific labeling at human chromosome band 17q21.3. Fluorescent signals were detected on chromosome 17 in each of 21 metaphase spreads scored. Of 83 signals observed, 34 (41%) were on 17q21.3. Paired (on sister chromatids) signals were only seen at band 17q21.3.

EXAMPLE III

Isolation of MOAT-E and MOAT-E cDNA.

Analysis of ara, a reported cDNA sequence that encodes a 453 amino acid transporter, revealed that it is a non-physiological sequence representing a combination of 5' MRP sequences fused to an MRP/cMOAT-related transporter. The MRP sequences extend to codon 8 of the reported predicted protein.

To isolate the complete physiological cDNA, a RT/PCR approach was employed in which primers were designed based upon a reported genomic sequence that encodes exons identical to the reported ara sequence. The MOAT-E cDNA was isolated in three segments. The first segment, spanning residues 1-616, was isolated by PCR using 5' primer ATGGCCGCGCCTGCTGAGC; (SEQ ID NO: 10)and 3' primer GTCTACGACACCAGGGTCAA (SEQ ID NO: 11). The second segment, spanning residues 1815-3187, was isolated by PCR using 5' CTGCCTGGAAGAAGTTGACC (SEQ ID NO: 12) and 3' primer CTGGAATGTCCACGTCAACC (SEQ ID NO: 13). The third segment, spanning residues 3158-1503, was isolated by PCR using 5' primer GGAGACAGACACGGTTGACG (SEQ ID NO: 14) and 3' primer GCAGACCAGGCCTGACTCC (SEQ ID NO: 15). The primer were designed based upon the nucleotide sequence of human genomic BAC clone CIT987SD-962B4. The template for these reactions was random-primed human kidney cDNA prepared from total RNA. Using this approach the physiological cDNA was isolated which is designated MOAT-E herein and set forth as Sequence I.D. No. 7.

Analysis of the MOAT-E Predicted Protein.

MOAT-E encodes a 1503 amino acid transporter. The MOAT-E predicted amino acid sequence is designated Sequence I.D. No. 8. See Figure 9. Also shown is the

location of potential transmembrane helices (overbars), potential N-glycosylation site (black dot) and the two nucleotide binding folds (NBF1 and NBF2). Walker A and B motifs, as well as the signature C motif of ABC transporters are also indicated. Comparison of MOAT-E with ara indicates that the ara predicted protein is not only a fused sequence, but also that it represents only 446 (~30%) of the 1503 MOAT-E residues.

Comparison of MOAT-E with the other members of the MRP/cMOAT subfamily, which include MRP, cMOAT, MOAT-B, MOAT-C and MOAT-E, is shown in Table IV. MOAT-E is highly related to MOAT-D, MRP and cMOAT, with which it shares 39-45% identity. This high degree of identity is also indicated by the high percent identities of the nucleotide binding folds, which range from 55-61%. In contrast, MOAT-E is less related to MOAT-B and MOAT-C, with which it shares ~31% and 34% identity, respectively.

Table IV. Amino acid identity among MRP/cMOAT sub-family members.[a] The bold type indicates the percent identity of the overall proteins, and the parentheses indicates the percent identity of the nucleotide binding folds.

	MOAT-E	MOAT-B	MOAT-C	MOAT-D	MRP	cMOAT
			% identity[b]			
MOAT-E	---	**33.9**	**30.6**	**43.6**	**45.1**	**38.9**
	---	(52.0/56.6)	(50.0/52.5)	(59.3/59.4)	(61.3/61.4)	(55.3/59.4)
MOAT-B	**33.9**	---	**36.4**	**35.3**	**39.4**	**36.8**
	(52.0/56.6)	---	(49.3/59.1)	(55.3/54.1)	(57.3/61.6)	(56.0/57 2)
MOAT-C	**30.0**	**36.4**	---	**33.1**	**35.8**	**36.2**
	(50.0/52.5)	(49.3/59.1)	---	(57.3/58.9)	(60.6/59.4)	(61.3/60.6)
MOAT-D	**43.6**	**35.3**	**33.1**	---	**57.3**	**46.9**
	(59.3/59.4)	(55.3/54.1)	(57.3/58.9)	---	(70 7/73.8)	(67.3/70.0)
MRP	**45.1**	**39.4**	**35.8**	**57.3**	---	**48.4**
	(61.3/61.9)	(57.3/61.6)	(60.0/59.4)	(70.7/73.8)	---	(66.0/73 1)
cMOAT	**38.9**	**36.8**	**36.2**	**46.9**	**48.4**	---
	(53.1/59.4)	(56.0/57.2)	(61.3/60.6)	(67.3/70.0)	(66.0/73.1)	---

[a]overall amino acid identifies are indicated in bold-face, and identities of nucleotide binding folds 1 and 2 are indicated in parentheses (NBF1/NBF2).
[b]percent identity was obtained using the GAP command in the GCG package.

Comparison of the hydropathy profile of MOAT-E with other members of the MRP/cMOAT subfamily if shown in figure 10. The data reveal that MOAT-E has a hydrophobic N-terminal segment that is present in its closest relatives, MOAT-D, MRP and cMOAT. This structural feature is present in all of the currently known organic anion transporters, and suggests that MOAT-E may share substrate specificity with MRP and cMOAT. MOAT-E may also share the drug resistance activity of the latter two proteins. In contrast, MOAT-B and MOAT-C do not have this hydrophobic N-terminal extension.

Expression Pattern of MOAT-E in Human Tissues.

In a Northern blot of RNA isolated from various tissues, MOAT-E expression is restricted to liver and kidney, suggesting that MOAT-E may participate the excretion of substances into the urine and bile. See Figure 11. This figure also shows that MOAT-E is expressed as an ~6 kB transcript. This is in contrast to the ~2.3 kB transcript that was reported for ara, clearly indicating that the fused ara transcript is unique to the cell line from which it was isolated, and is not a physiological transcript. Together, the isolation of MOAT-E and analysis of its sequence and expression pattern suggest that it may be involved in cellular resistance to drugs and/or the excretion of drugs into the urine and bile.

DISCUSSION

The present invention discloses additional MRP/cMOAT-related transporters which were identified by

using a degenerative PCR cloning approach in which the conserved amino terminal ATP-binding domain of known eukaryotic transporters was targeted. Using this approach the complete coding sequences of MOAT-B, MOAT-C, MOAT-D and MOAT-E were obtained. MOAT-B is a protein whose predicted structure indicates that it is a member of the ABC transporter family. Comparison of the MOAT-B predicted protein with other transporters reveals that it is most closely related to MRP, cMOAT and yeast YCF1, and thus extends the number of known full length MRP-related transporters. The similarity of MOAT-B to these transporters suggest that it shares a similar substrate specificity. Transport assays using membrane vesicle preparations indicate that MRP is capable of transporting diverse organic anions, including glutathione S-conjugates such as LTC_4, oxidized glutathione, and glucuronidated and sulfated conjugates of steroid hormones and bile salts (7). Although membrane vesicle transport assays of substrate specificity using cMOAT-transfected cells have not yet been reported, genetic and biochemical studies using TR- and EHBR rat strains, which are defective in the hepatobiliary excretion of glutathione and glucuronate conjugates, indicate that it is also an ATP-dependent transporter of organic anions. cMOAT, which is primarily expressed in the canalicular membrane of hepatocytes, has been reported to be absent in these rat strains, and hepatocyte canalicular membranes prepared from the mutant rats are deficient in the ATP-dependent transport of glutathione and glucuronate conjugates (23, 24). In addition, cMOAT protein has also been reported to be absent in the hepatocytes of patients with Dubin-Johnson syndrome (25), a disorder manifested by chronic

conjugated hyperbilirubinemia. YCF1, a yeast transporter, has also been demonstrated to transport glutathione complexes (26). Thus, based upon the similarity of MOAT-B to these three transporters, it is possible that it also functions to transport organic anions, an activity critical to the cellular detoxification of a wide range of xenobiotics.

MOAT-C, MOAT-D and MOAT-E are three other MRP/cMOAT-related transporters. The isolation of these two transporters extends the number of known full length members of this subfamily to six. Based upon the degree of amino acid similarity and overall topology these six proteins fall into two groups. The first group is composed of MOAT-D, MOAT-E, MRP and cMOAT. These four transporters are highly related, sharing ~39-45% amino acid identity. MOAT-D is more closely related to MRP (57% identity) than is cMOAT (48% identity), and is therefore the closest known relative of MRP. In addition to a high degree of amino acid identity, the similarity between MOAT-D, MRP and cMOAT, also extends to overall topology. Like MRP and cMOAT, MOAT-D and MOAT-E have three membrane spanning domains, including an N-terminal hydrophobic extension that is predicted to harbor ~5 transmembrane helices, and which is absent in transporters such as CFTR and MDR1. This N-terminal extension is also present in YCF1, a related yeast transporter that transports glutathione S-conjugates, and SUR, a more distantly related transporter involved in the regulation of potassium channels. The second group of MRP/cMOAT-related transporters is composed of MOAT-B and MOAT-C. These two transporters are distinguished from the first group by their lower level of amino acid similarity and distinct topology. Like MOAT-D and MOAT-E, MOAT-B

and MOAT-C are more closely related to MRP (39% and 36%, respectively) and cMOAT (37% and 36%, respectively) than to other eukaryotic transporters . However, they share considerably less similarity with MRP, cMOAT, MOAT-D and MOAT-E than the latter four transporters share with each other (~39-45% identity). In addition, in contrast to MRP, cMOAT, MOAT-D and MOAT-E, MOAT-B and MOAT-C do not have an N-terminal membrane spanning domain, and their topology is therefore more similar to many other eukaryotic ABC transporters that also have only two membrane spanning domains.

Defining the contributions of MOAT-B, MOAT-C, MOAT-D and MOAT-E to cytotoxic drug resistance will facilitate the design of novel chemotherapeutic agents. The multidrug resistance activity of MRP is well described. While the drug sensitivity pattern of cMOAT-transfected cells has not yet been reported, the possibility that it may also confer resistance to cytotoxic drugs is suggested by a recent report in which transfection of a cMOAT antisense vector was found to enhance the sensitivity of a human liver cancer cell line to both natural product drugs and cisplatin. Since MOAT-D and MOAT-E are more closely related to MRP than is cMOAT, the possibility that they will also confer resistance is particularly intriguing. The availability of the MOAT-B, MOAT-C, MOAT-D and MOAT-E cDNAs will facilitate the analysis of their possible contributions to cytotoxic resistance.

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While certain of the preferred embodiments of the present invention have been described and specifically exemplified above, it is not intended that the invention be limited to such embodiments. Various modifications may be made thereto without departing from the scope and spirit of the present invention, as set forth in the following claims.

What is claimed is:

1. An isolated nucleic acid molecule having the sequence of SEQ ID NO:1, said nucleic acid molecule comprising a nucleotide sequence encoding a MOAT-B transporter protein about 1350 amino acids in length, said encoded transporter protein comprising a multi-domain structure including a tandem repeat of nucleotide binding folds appended C-terminal to a hydrophobic domain, said nucleotide binding folds having Walker A and B ATP binding sites, said C-terminal domain having a plurality of membrane spanning helices.

2. The nucleic acid molecule of claim 1, which is DNA.

3. The DNA molecule of claim 2, which is a cDNA comprising a sequence approximately 5.9 kilobase pairs in length that encodes said MOAT-B transporter protein.

4. The DNA molecule of claim 2, which is a gene comprising introns and exons, the exons of said gene specifically hybridizing with the nucleic acid of SEQ ID NO 1, and said exons encoding said MOAT-B transporter protein.

5. An isolated RNA molecule transcribed from the nucleic acid of claim 1.

6. The nucleic acid molecule of claim 1, wherein said sequence encodes a MOAT-B transporter

protein having an amino acid sequence selected from the group consisting of SEQ ID NO 2 and amino acid sequences encoded by natural allelic variants of said sequence.

7. The nucleic acid molecule of claim 6, which comprises SEQ ID NO 1.

8. An antibody immunologically specific for the protein encoded by the nucleic acid of claim 1.

9. An antibody as claimed in claim 8, said antibody being monoclonal.

10. An antibody as claimed in claim 8, said antibody being polyclonal.

11. An isolated nucleic acid molecule having the sequence of SEQ ID NO: 3, said nucleic acid molecule comprising a sequence encoding a MOAT-C transporter protein about 1450 amino acids in length, said transporter protein having a multi-domain structure including a tandem repeat of nucleotide binding folds, said nucleotide binding foldes having Walker A and B binding sites, and a C-terminal hydrophobic domain that contains several membrane spanning helices.

12. The nucleic acid molecule of claim 11, which is DNA.

13. The DNA molecule of claim 12, which is a cDNA comprising a sequence approximately 6.6 kilobase pairs in length that encodes said MOAT-C transporter protein.

14. The DNA molecule of claim 12, which is a gene comprising introns and exons, the exons of said gene specifically hybridizing with the nucleic acid of SEQ ID NO 3, and said exons encoding said MOAT-C transporter protein.

15. An isolated RNA molecule transcribed from the nucleic acid of claim 11.

16. The nucleic acid molecule of claim 11, wherein said sequence encodes a MOAT-C transporter protein having an amino acid sequence selected from the group consisting of SEQ ID NO 4 and amino acid sequences encoded by natural allelic variants of said sequence.

17. The nucleic acid molecule of claim 11, which comprises SEQ ID NO 3.

18. An antibody immunologically specific for the protein encoded by the nucleic acid of claim 11.

19. An antibody as claimed in claim 18, said antibody being monoclonal.

20. An antibody as claimed in claim 18, said antibody being polyclonal.

21. An oligonucleotide between about 10 and about 200 nucleotides in length, which specifically hybridizes with a protein translation initiation site in a nucleotide sequence encoding amino acids of SEQ ID NO 4.

22. An oligonucleotide between about 10 and about 200 nucleotides in length, which specifically hybridizes with a protein translation initiation site in a nucleotide sequence encoding amino acids of SEQ ID NO 2.

23. An isolated nucleic acid molecule having the sequence of SEQ ID NO: 5, said nucleic acid molecule comprising a sequence encoding a MOAT-D transporter protein about 1550 amino acids in length, said transporter protein having a multi-domain structure including a tandem repeat of nucleotide binding folds, said nucleotide binding foldes having Walker A and B binding sites, and a C-terminal hydrophobic domain that contains several membrane spanning helices.

24. The nucleic acid molecule of claim 23, which is DNA.

25. The DNA molecule of claim 24, which is a cDNA comprising a sequence approximately 6 kilobase pairs in length that encodes said MOAT-D transporter protein.

26. The DNA molecule of claim 24, which is a gene comprising introns and exons, the exons of said gene specifically hybridizing with the nucleic acid of SEQ ID NO 5, and said exons encoding said MOAT-D transporter protein.

27. An isolated RNA molecule transcribed from the nucleic acid of claim 23.

28. The nucleic acid molecule of claim 23, wherein

said sequence encodes a MOAT-D transporter protein having an amino acid sequence selected from the group consisting of SEQ ID NO 6 and amino acid sequences encoded by natural allelic variants of said sequence.

29. The nucleic acid molecule of claim 23, which comprises SEQ ID NO 5.

30. An antibody immunologically specific for the protein encoded by the nucleic acid of claim 23.

31. An antibody as claimed in claim 30, said antibody being monoclonal.

32. An antibody as claimed in claim 30, said antibody being polyclonal.

33. An oligonucleotide between about 10 and about 200 nucleotides in length, which specifically hybridizes with a protein translation initiation site in a nucleotide sequence encoding amino acids of SEQ ID NO 6.

34. An isolated nucleic acid molecule having the sequence of SEQ ID NO:7, said nucleic acid molecule comprising a nucleotide sequence encoding a MOAT-E transporter protein about 1503 amino acids in length, said transporter protein having a multi-domain structure including a tandem repeat of nucleotide binding folds, said nucleotide binding folds having Walker A and B binding sites, and a C-terminal hydrophobic domain that contains several membrane spanning helices.

35. The nucleic acid molecule of claim 34,

which is DNA.

36. The DNA molecule of claim 35, which is a cDNA comprising a sequence approximately 6 kilobase pairs in length that encodes said MOAT-E transporter protein.

37. The DNA molecule of claim 35, which is a gene comprising introns and exons, the exons of said gene specifically hybridizing with the nucleic acid of SEQ ID NO 7, and said exons encoding said MOAT-E transporter protein.

38. An isolated RNA molecule transcribed from the nucleic acid of claim 34.

39. The nucleic acid molecule of claim 34, wherein said sequence encodes a MOAT-E transporter protein having an amino acid sequence selected from the group consisting of SEQ ID NO 8 and amino acid sequences encoded by natural allelic variants of said sequence.

40. The nucleic acid molecule of claim 39, which comprises SEQ ID NO 7.

41. An antibody immunologically specific for the protein encoded by the nucleic acid of claim 34.

42. An antibody as claimed in claim 41, said antibody being monoclonal.

43. An antibody as claimed in claim 41, said antibody being polyclonal.

44. An oligonucleotide between about 10 and about 200 nucleotides in length, which specifically hybridizes with a protein translation initiation site in a nucleotide sequence encoding amino acids of SEQ ID NO 7.

45. A plasmid comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5 and SEQ ID NO:7.

46. A vector comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5 and SEQ ID NO:7.

47. A retroviral vector comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5 and SEQ ID NO:7.

48. A host cell comprising at least one nucleic acid molecule having a sequence selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5 and SEQ ID NO:7.

49. A host cell as claimed in claim 48, wherein said host cell is selected from the group consisting of bacterial, fungal, mammalian, insect and plant cells.

50. A host cell as claimed in claim 48, wherein said nucleic acid is provided in a plasmid and is operably linked to mammalian regulatory elements which confer high expression and stability of mRNA transcribed from said nucleic acid.

51. A host cell as claimed in claim 48, wherein said nucleic acid is provided in a plasmid and is operably linked to mammalian regulatory control elements in reverse anti-sense orientation.

52. A host animal comprising at least one nucleic acid molecule selected from the group consisting of SEQ ID NO: 1, SEQ ID NO: 3, SEQ ID NO: 5 and SEQ ID NO: 7.

53. A host animal as claimed in claim 52, wherein said animal harbors a homozygous null mutation in its endogenous MOAT gene wherein said mutation has been introduced into said mouse or an ancestor of said mouse via homologous recombination in embryonic stem cells, and further wherein said mouse does not express a functional mouse MOAT protein.

54. The transgenic mouse of claim 53, wherein said mouse is fertile and transmits said null mutation to its offspring.

55. The transgenic mouse of claim 53, wherein said null mutation has been introduced into an ancestor of said mouse at an embryonic stage following microinjection of embryonic stem cells into a mouse blastocyt.

56. A method for screening a test compound for inhibition of MOAT mediated transport, comprising:

a) providing a host cell expressing at least one MOAT-encoding nucleic acid having a sequence selected from the group consisting of SEQ ID NOS: 1, 3, 5, and 7;

b) contacting said host cell with a compound suspected of inhibiting MOAT-mediated transporter activity; and

c) assessing inhibition of transport mediated by said compound.

57. A method as claimed in claim 56, wherein inhibition of MOAT mediated transport is indicated by restoration of anticancer drug sensitivity.

58. A method as claimed in claim 57, wherein said inhibition of MOAT mediated transport is indicated by a reduction of transporter mediated cellular efflux of anticancer agents.

59. A kit for detecting the presence of MOAT encoding nucleic acids in a sample, comprising:

a) oligonucleotide primers specific for amplification of MOAT encoding nucleic acids;

b) polymerase enzyme;

c) amplification buffer; and

d) MOAT specific DNA for use as a positive control.

```
MOAT-B          ....................................................................................................
MRP          1  MALRGFCSADGSDPLWDWNVTWNTSNPDFTKCFQNTVLVWVPCFYLWACFPFYFLYLSRHDRGYIQMTPLNKTKTALGFLLWIVCWADLFYSFWERSRGI 100
MOAT-B       1  .................................................................................................MLP 3
MRP        101  FLAPVFLVSPTLLGITTLLATFLIQLERRKGVQSSGIMLTFWLVALVCALAILRSKIMTALKEDAQVDLFRDITFYVYFSLLLIQLVLSCFSDRSPLFSE 200
MOAT-B       4  VYQEVKPNPLQDANICSRVFFWWLNPLFKIGHKRRLEEDDMYSVLPEDRSQHLGEELQGFWDKEVLRAENDAQK.......................... 77
MRP        201  TIHDPNPCPESSASFLSRITFWWITGLIVRGYRQPLEGSDLWSLNKEDTSEQVVPVLVKNWKKECAKTRKQPVKVVYSSKDPAQPKESSKVDANEEVEAL 300
MOAT-B      78  ..........PSLTRAIIKCYWKSYLVLGIFTLIEESAKVIQPIFLGKIINYFENYDPMDSVALNTAYAYATVLTFCTLIL.AILHHLYFYHVQCAGMRL 166
MRP        301  IVKSPQKEWNPSLFKVLYKTFGPYFLMSFFFKAIHDLMMFSGPQILKLLIKFVNDTKAPDWQGY.....FYTVLLFVTACLQTLVLHQYFHICFVSGMRI 395
MOAT-B     167  RVAMCHMIYRKALRLSNMAMGKTTTGQIVNLLSNDVNKFDQVTVFLHFLWAGPLQAIAVTALLWMEIGISCLAGMAVLIILLPLQSCFGKLFSSLRSKTA 266
MRP        396  KTAVIGAVYRKALVITNSARKSSTVGEIVNLMSVDAQRFMDLATYINMIWSAPLQVILALYLLWLNLGPSVLAGVAVMVLMVPVNAVMAMKTKTYQVAHM 495
MOAT-B     267  TFTDARIRTMNEVITGIRIIKMYAWEKSFSNLITNLRKKEISKILRSSCLRGMNLASFFSASKIIVFVTFTTYVLLG..SVITASRVFVAVTLYGAVRLT 364
MRP        496  KSKDNRIKLMNEILNGIKVLKLYAWELAFKDKVLAIRQEELKVLKKSAYLSAVGTFTWVCTPFLVALCTFAVYVTIDENNILDAQTAFVSLALFNILRFP 595
                                                                                              NBF1
MOAT-B     365  VTLFFPSAIERVSEAIVSIRRIQTFLLLDEIS....QRNRQLPSDGKKMVHVQDFTAFWDKASETPTLQGLSFTVRPGELLAVVGPVGAGKSSLLSAVLG 460
MRP        596  LNI.LPMVISSIVQASVSLKRLRIFLSHEELEPDSIERRPVKDGGGTNSITVRNATFTWAR.SDPPTLNGITFSIPEGALVAVVGQVGCGKLSLLSALLA 693
MOAT-B     461  ELAPSHGLVSVHGRIAYVSQQPWVFSGTLRSNILFGKKYEKERYEKVIKACALKKDLQLLEDGDLTVIGDRGTTLSGGQKARVNLARAVYQDADIYLLDD 560
MRP        694  EMDKVEGHVAIKGSVAYVPQQAWIQNDSLRENILFGCQLEEPYYRSVIQACALLPDLEILPSGDRTEIGEKGVNLSGGQKQRVSLARAVYSNADIYLFDD 793
                      NBF1
MOAT-B     561  PLSAVDAEVSRHLFELCICQ..ILHEKITILVTHQLQYLKAASQILILKDGKMVQKGTYTEFLKSGIDFGSLLK........KDNEESEQPPVPG..... 645
MRP        794  PLSAVDAHVGKHIFENVIGPKGMLKNKTRILVTHSMSYLPQVDVIIVMSGGKISEMGSYQELLARDGAFAEFLRTYASTEQEQDAEENGVTGVSGPGKEA 893
MOAT-B     646  ............TPTLRNRTFSESSVWSQQSSRPSLKDGALESQDT..ENVPVTLSEENRSEGKVGFQAYKNYFRAGAHWIVFIFLILLNTAAQVAYVLQ 731
MRP        894  KQMENGMLVTDSAGKQLQRQLSSSSSYSGDISRHHNSTAELQKAEAKKEETWKLMEADKAQTGQVKLSVYWDYMKAIGLFISFLSIFLF.MCNHVSALAS 992
MOAT-B     732  DWWLSYWANKQSMLNVTVNGGGNVTEKLDLNWYLGIYSGLTVATVLFGIARSLLVFYVLVNSSQTLHNKMFESILKAPVLFFDRNPIGRILNRFSKDIGH 831
MRP        993  NYWLSLWTD.....DPIVNGTQEHTKVR.....LSVYGALGISQGIAVFGYSMAVSIGGILASRCLHVDLLHSILRSPMSFFERTPSGNLVNRFSKELDT 1082
MOAT-B     832  LDDLLPLTFLDFIQTLLQVVGVVSVAVAVIPWIAIPLVPLGIIFIFLRRYFLETSRDVKRLESTTRSPVFSHLSSSLQGLWTIRAYKAEERCQELFDAHQ 931
MRP       1083  VDSMIPEVIKMFMGSLFNVIGACIVILLATPIAAIIIPPLGLIYFFVQRFYVASSRQLKRLESVSRSPVYSHFNETLLGVSVIRAFEEQERFIHQSDLKV 1182
MOAT-B     932  DLHSEAWFLFLTTSRWFAVRLDAICAMFVIIVAFGSLILAKTLDAGQVGLALSYALTLMGMFQWCVRQSAEVENMMISVERVIEYTDLEKEAPWEYQK.R 1030
MRP       1183  DENQKAYYPSIVANRWLAVRLECVGNCIVLFAALFAVISRHSLSAGLVGLSVSYSLQVTTYLNWLVRMSSEMETNIVAVERLKEYSETEKEAPWQIQETR 1282
                                                NBF2
MOAT-B    1031  PPPAWPHEGVIIFDNVNFMYSPGGPLVLKHLTALIKSQEKVGIVGRTGAGKSSLISALFRLSE.PEGKIWIDKILTTEIGLHDLRKKMSIIPQEPVLFTG 1129
MRP       1283  PPSSWPQVGRVEFRNYCLRYREDLDFVLRHINVTINGGEKVGIVGRTGAGKSSLTLGLFRINESAEGEIIIDGINIAKIGLHDLRFKITIIPQDPVLFSG 1382
                                                                                                       NBF2
MOAT-B    1130  TMRKNLDPFKEHTDEELWNALQEVQLKETIEDLPGKMDTELAESGSNFSVGQRQLVCLARAILRKNQILIIDEATANVDPRTDELIQKKIREKFAHCTVL 1229
MRP       1383  SLRMNLDPFSQYSDEEVWTSLELAHLKDFVSALPDKLDHECAEGGENLSVGQRQLVCLARALLRKTKILVLDEATAAVDLETDDLIQSTIRTQFEDCTVL 1482
MOAT-B    1230  TIAHRLNTIIDSDKIMVLDSGRLKEYDEPYVLLQNKESLFYKMVQQLGKAEAAALTETAKQVYFKRNYHIGHTDHMVTNTSNGQPSTLTIFETAL 1325
MRP       1483  TIAHRLNTIMDYTRVIVLDKGEIQEYGAPSDLLQQR.GLFYSMAKDAGLV 1531
```

Figure 1

Fig. 2A

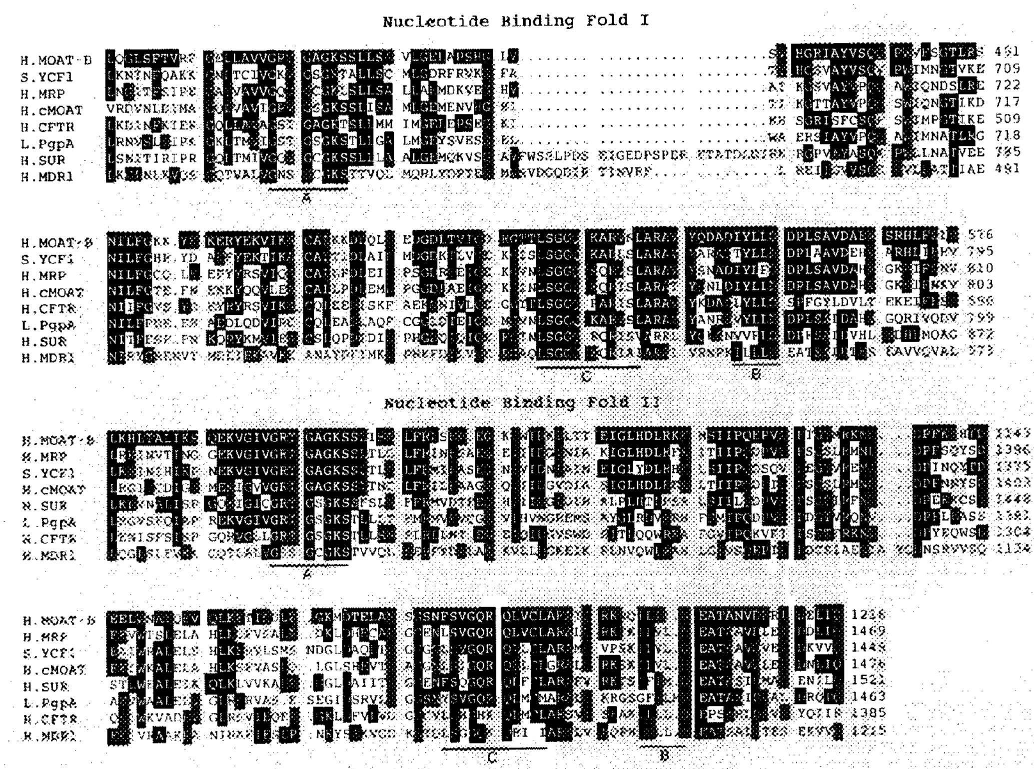
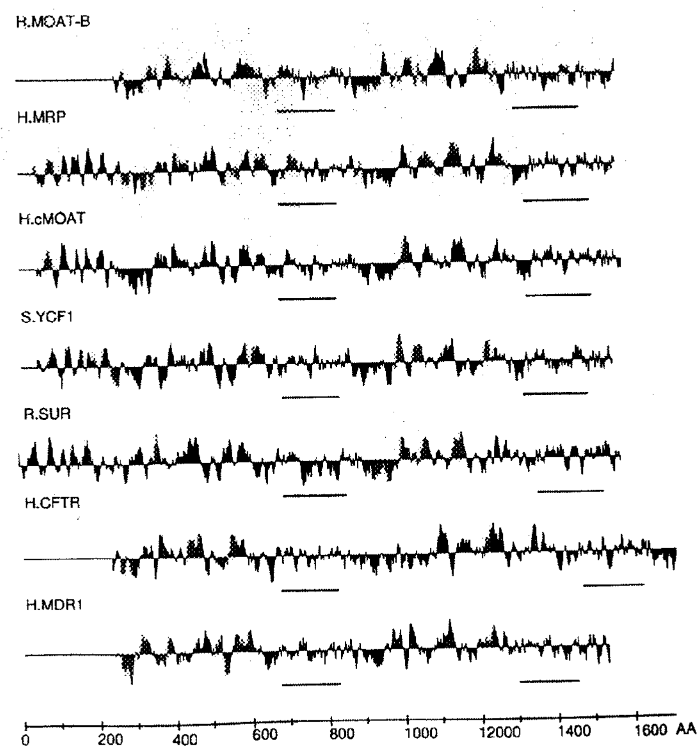

Nucleotide Binding Fold I
H.MOAT-B
S.YCF1
H.MRP
H.cMOAT
H.CFTR
L.PgpA
H.SUR
H.MDR1
Nucleotide Binding Fold II

Fig. 2B


H.MOAT-B
H.MRP
H.cMOAT
S.YCF1
R.SUR
H.CFTR
H.MDR1
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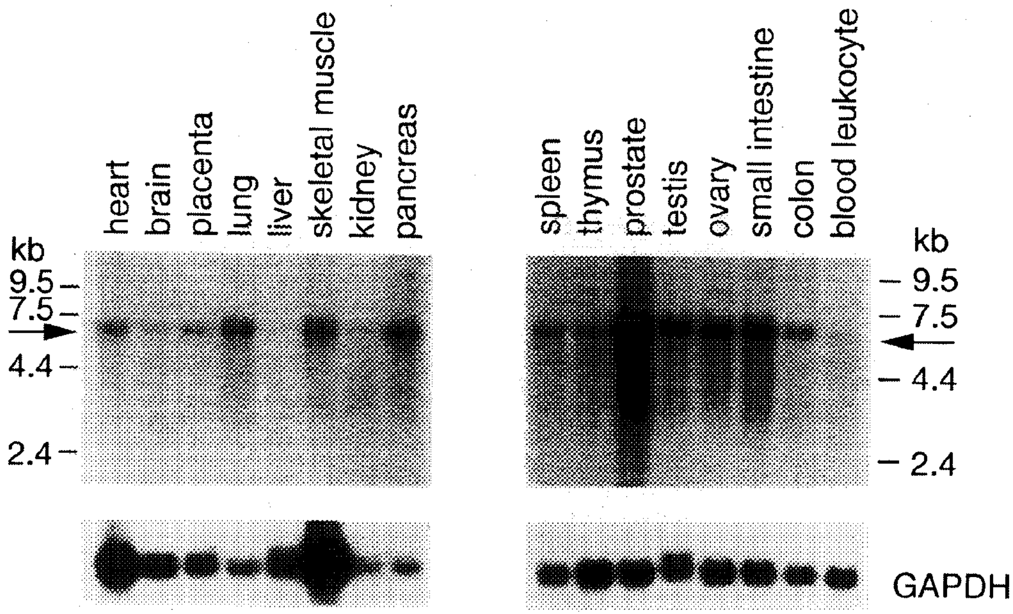
400
600
800
1000
12000
1400
1600 AA


heart
brain
placenta
lung
liver
skeletal muscle
kidney
pancreas
spleen
thymus
prostate
testis
ovary
small intestine
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kb
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7.5
4.4
2.4
GAPDH

Figure 3

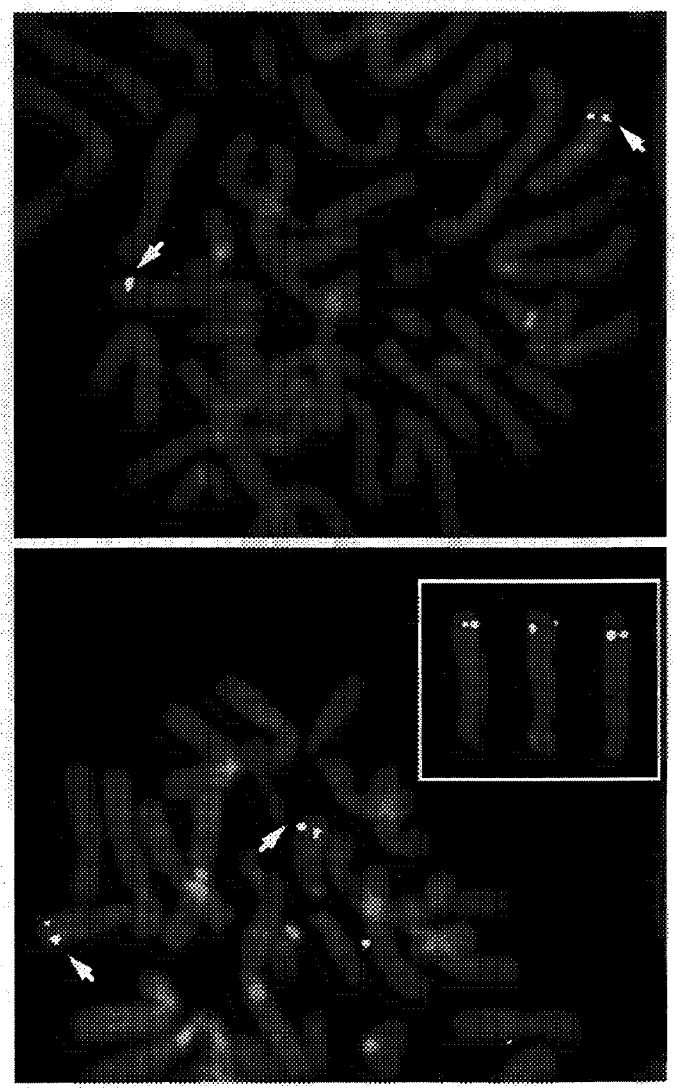

Figure 4

Fig. 5A

1 MKDIDIGKEY IIPSPGYRSV RERTSTSGTH RDREDSKFRR TRPLECQDAL ETAARAEGLS

61 LDASMHSQLR ILDEEHPKGK YHHGLSALKP IRTTSKHQHP VDNAGLFSCM TFSWLSSLAR

121 VAHKKGELSM EDVWSLSKHE SSDVNCRRLE RLWQEELNEV GPDAASLRRV VWIFCRTRLI

TM1 TM2

181 LSIVCLMITQ LAGFSGPAFM VKHLLEYTQA TESNLQYSLL LVLGLLLTEI VRSWSLALTW

TM3

241 ALNYRTGVRL RGAILTMAFK KILKLKNIKE KSLGELINIC SNDGQRMFEA AAVGSLLAGG

TM4

301 PVVAILGMIY NVIILGPTGF LGSAVFILFY PAMMFASRLT AYFRRKCVAA TDERVQKMNE

TM5

361 VLTYIKFIKM YAWVKAFSQS VQKIREEERR ILEKAGYFQG ITVGVAPIVV VIASVVTFSV

TM6

421 HMTLGFDLTA AQAFTVVTVF NSMTFALKVT PFSVKSLSEA SVAVDRFKSL FLMEEVHMIK

481 NKPASPHIKI EMKNATLAWD SSHSSIQNSP KLTPKMKKDK RASRGKKEKV RQLQRTEHQA

NBF1

541 VLAEQKGHLL LDSDERPSPE EEEGKHIHLG HLRLQRTLHS IDLEIQEGKL VGICGSVGSG

A

601 KTSLISAILG QMTLLEGSIA ISGTFAYVAQ QAWILNATLR DNILFGKEYD EERYNSVLNS

661 CCLRPDLAIL PSSDLTEIGE RGANLSGGQR QRISLARALY SDRSIYILDD PLSALDAHVG

NBF1 C B

721 NHIFNSAIRK HLKSKTVLFV THQLQYLVDC DEVIFMKEGC ITERGTHEEL MNLNGDYATI

781 FNNLLLGETP PVEINSKKET SGSQKKSQDK GPKTGSVKKE KAVKPEEGQL VQLEEKGQGS

TM7

841 VPWSVYGVYI QAAGGPLAFL VIMALFMLNV GSTAFSTWWL SYWIKQGSGN TTVTRGNETS

TM8

901 VSDSMKDNPH MQYYASIYAL SMAVMLILKA IRGVVFVKGT LRASSRLHDE LFRRILRSPM

TM9

961 KFFDTTPTGR ILNRFSKDMD EVDVRLPFQA EMFIQNVILV FFCVGMIAGV FPWFLVAVGP

TM10

1021 LVILFSVLHI VSRVLIRELK RLDNITQSPF LSHITSSIQG LATIHAYNKG QEFLHRYQEL

TM11 TM12

1081 LDDNQAPFFL FTCAMRWLAV RLDLISIALI TTTGLMIVLM HGQIPPAYAG LAISYAVQLT

1141 GLFQFTVRLA SETEARFTSV ERINHYIKTL SLEAPARIKN KAPSPDWPQE GEVTFENAEM

NBF2

1201 RYRENLPLVL KKVSFTIKPK EKIGIVGRTG SGKSSLGMAL FRLVELSGGC IKIDGVRISD

A

1261 IGLADLRSKL SIIPQEPVLF SGTVRSNLDP FNQYTEDQIW DALERTHMKE CIAQLPLKLE

NBF2

1321 SEVMENGDNF SVGERQLLCI ARALLRHCKI LILDEATAAM DTETDLLIQE TIREAFADCT

C B

1381 MLTIAHRLHT VLGSDRIMVL AQGQVVEFDT PSVLLSNDSS RFYAMFAAAE NKVAVKG

Fig. 5B

```
                                                                        TM1
1    MGPMDALCGS GELGSKFWDS NLSVHTENPD LTPCFQNSLL AWVPCIYLWV ALPCYLLYLR
                                    TM2
61   HHCRGYIILS HLSKLKMVLG VLLWCVSWAD LFYSFHGLVH GRAPAPVFFV TPLVVGVTML
     TM3                            TM4
121  LATLLIQYER LQGVQSSGVL IIFWFLCVVC AIVPFRSKIL LAKAEGEISD PFRFTTFYIH
         TM5
181  FALVLSALIL ACFREKPPFF SAKNVDPNPY PETSVGFLSR LFFWWFTKMA IYGYRHPLEE

241  KDLWSLKEED RSQMVVQQLL EAWRKQEKQT ARHKASAAPG KNASGEDEVL LGARPRPRKP
                         TM6
301  SFLKALLATF GSSFLISACF KLIQDLLSFI NPQLLSILIR FISNPMAPSW WGFLVAGLMF
         TM7
361  LCSMMQSLIL QHYYHYIFVT GVKFRTGIMG VIYRKALVIT NSVKRASTVG EIVNLMSVDA
                         TM8                            TM9
421  QRFMDLAPFL NLLWSAPLQI ILAIYFLWQN LGPSVLAGVA FMVLLIPLNG AVAVKMRAFQ

481  VKQMKLKDSR IKLMSEILNG IKVLKLYAWE PSFLKQVEGI RQGELQLLRT AAYLHTTTTF
             TM10                              TM11
541  TWMCSPFLVT LITLWVYVYV DPNNVLDAEK AFVSVSLFNI LRLPLNMLPQ LISNLTQASV
                                                          NBF1
601  SLKRIQQFLS QEELDPQSVE RKTISPGYAI TIHSGTFTWA QDLPPTLHSL DIQVPKGALV

661  AVVGPVGCGK SSLVSALLGE MEKLEGKVHM KGSVAYVPQQ AWIQNCTLQE NVLFGKALNP
         A
721  KRYQQTLEAC ALLADLEMLP GGDQTEIGEK GINLSGGQRQ RVSLARAVYS DADIFLLDDP
                NBF1                        C                        B
781  LSAVDSHVAK HIFDHVIGPE GVLAGKTRVL VTHGISFLPQ TDFIIVLADG QVSEMGPYPA

841  LLQRNGSFAN FLCNYAPDED QGHLEDSWTA LEGAEDKEAL LIEDTLSNHT DLTDNDPVTY

901  VVQKQFMRQL SALSSDGEGQ GRPVPRRHLG PSEKVQVTEA KADGALTQEE KAAIGTVELS
                    TM12
961  VFWDYAKAVG LCTTLAICLL YVGQSAAAIG ANVWLSAWTN DAMADSRQNN TSLRLGVYAA
         TM13
1021 LGILQGFLVH LAAMAMAAGG IQAARVLHQA LLHNKIRSPQ SFFDTTPSGR ILNCFSKDIY
                     TM14                            TM15
1081 VVDEVLAPVI LMLLNSFFNA ISTLVVIMAS TPLFTVVILP LAVLYTLVQR FYAATSRQLK

1141 RLESVSRSPI YSHFSETVTG ASVIRAYNRS RDFEIISDTK VDANQRSCYP YIISNRWLSI
         TM16                                TM17
1201 GVEFVGNCVV LFAALFAVIG RSSLNPGLVG LSVSYSLQVT FALNWMIRMM SDLESNIVAV
                                                         NBF2
1261 ERVKEYSKTE TEAPWVVEGS RPPEGWPPRG EVEFRNYSVR YRPGLDLVLR DLSLHVHGGE

1321 KVGIVGRTGA GKSSMTLCLF RILEAAKGEI RIDGLNVADI GLHDLRSQLT IIPQDPILFS
             A
1381 GTLRMNLDPF GSYSEEDIWW ALELSHLHTF VSSQPAGLDF QCSEGGENLS VGQRQLVCLA
                            NBF2                            C
1441 RALLRKSRIL VLDEATAAID LETDNLIQAT IRTQFDTCTV LTIAHRLNTI MDYTRVLVLD
              B
1501 KGVVAEFDSP ANLIAARGIF YGMARDAGLA
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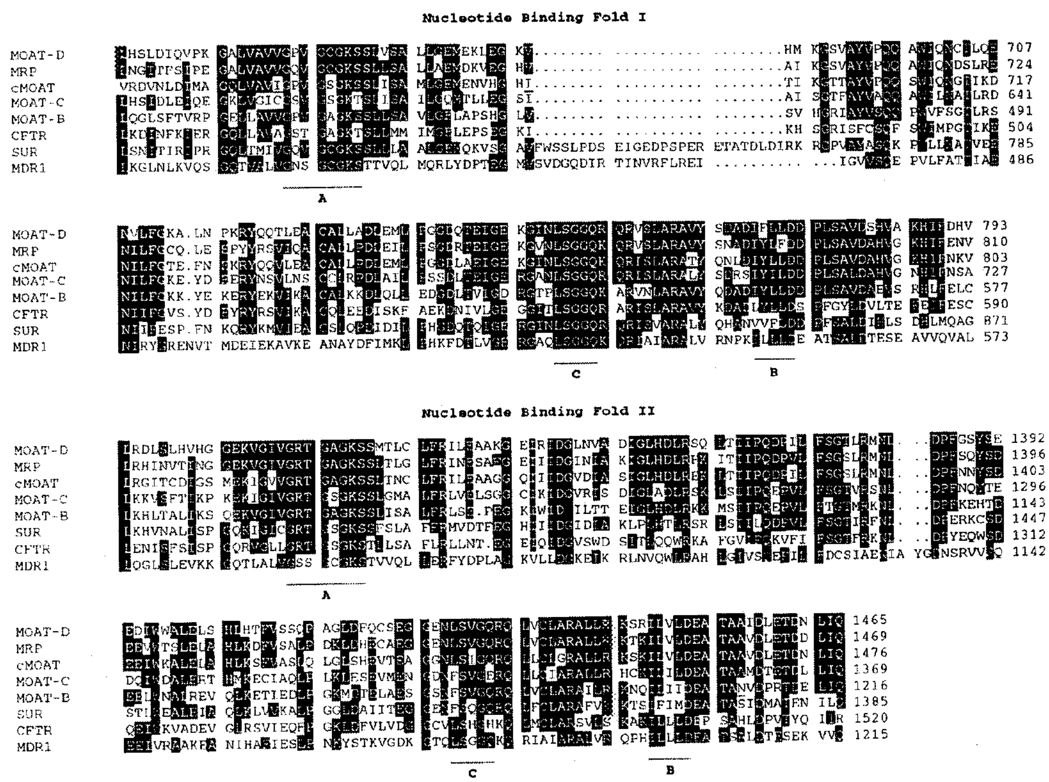
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MRP
cMOAT
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MOAT-B
CFTR
SUR
MDR1
A
C
B
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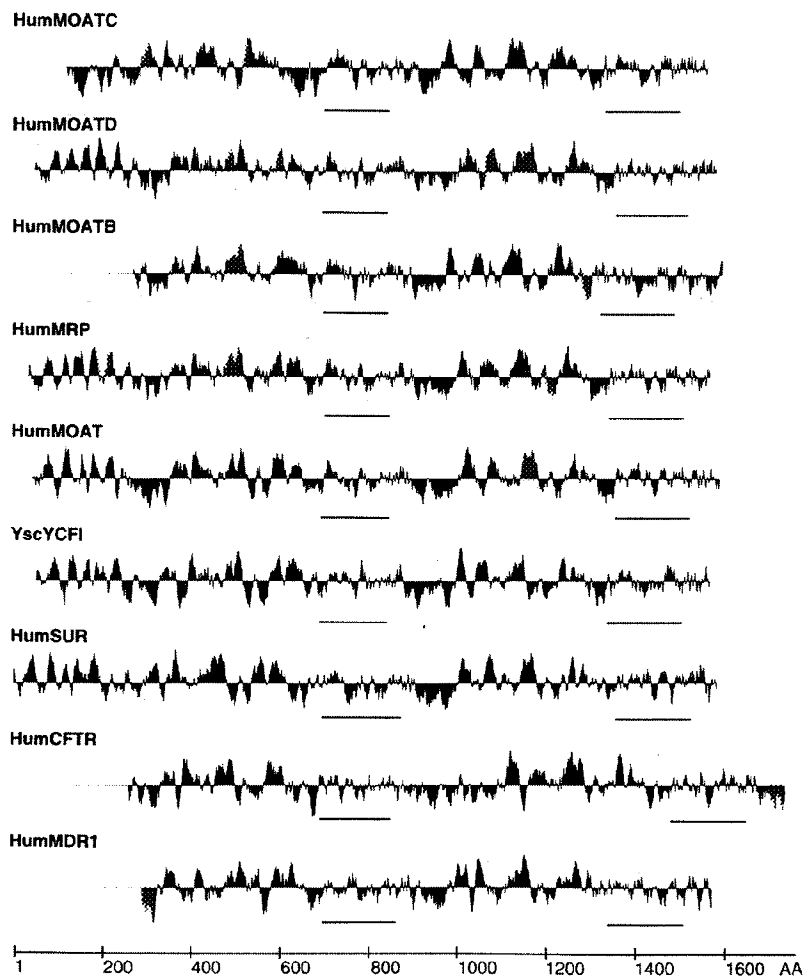
MRP
cMOAT
MOAT-C
MOAT-B
SUR
CFTR
MDR1
A
C
B

Fig. 6A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HumMOATD
HumMOATB
HumMRP
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HumCFTR
HumMDR1
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200
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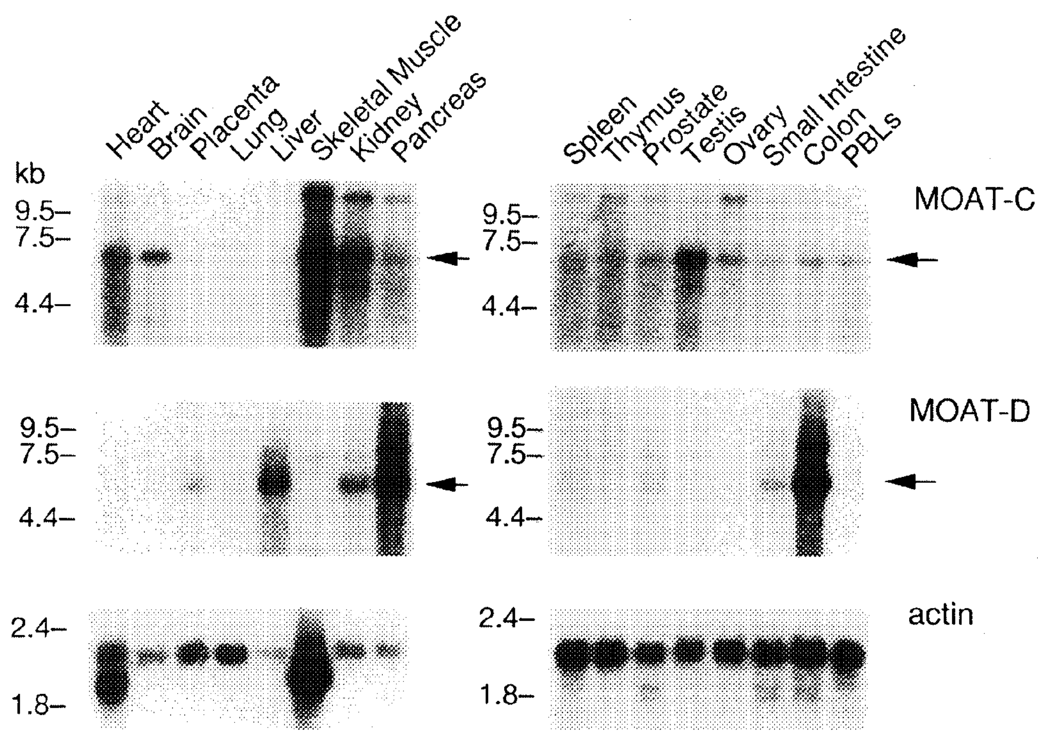
1200
1400
1600 AA

Fig. 6B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Brain
Placenta
Lung
Liver
Skeletal Muscle
Kidney
Pancreas
Spleen
Thymus
Prostate
Testis
Ovary
Small Intestine
Colon
PBLs
kb
9.5–
7.5–
4.4–
2.4–
1.8–
MOAT-C
MOAT-D
actin

Figure 7

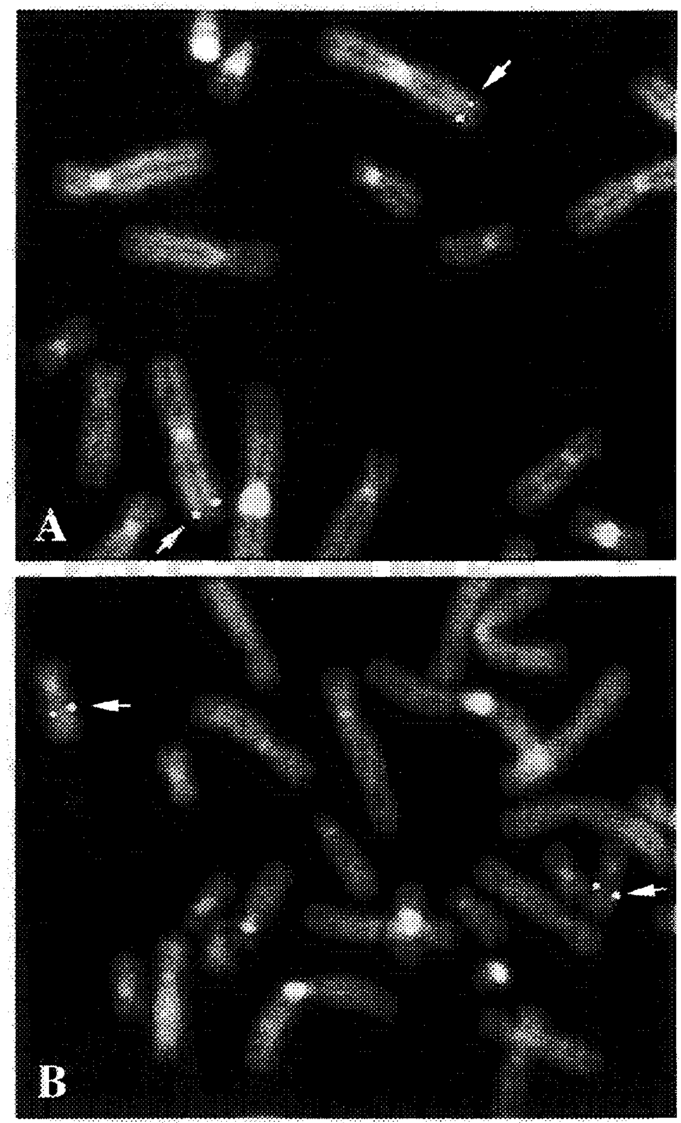
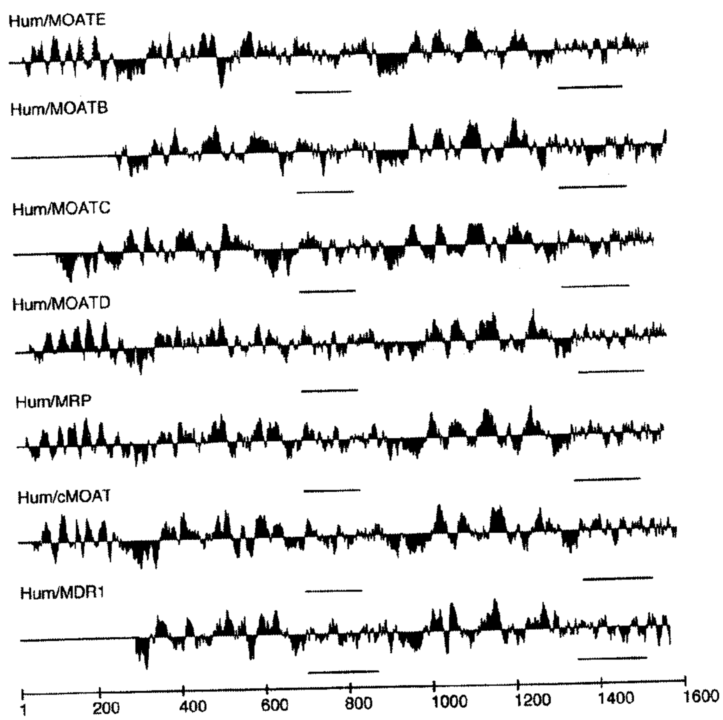


Figure 8

```
1    MAAPAEPCAG QGVWNQTEPE PAATSLLSLC FLRTAGVWVP PMYLWVLGPI YLLFIHHHGR
61   GYLRMSPLFK AKMVLGFALI VLCTSSVAVA LWKIQQGTPE APEFLIHPTV WLTTMSFAVF
121  LIHTERKKGV QSSGVLFGYW LLCFVLPATN AAQQASGAGF QSDPVRHLST YLCLSLVVAQ
181  FVLSCLADQP PFFPEDPQQS NPCPETGAAF PSKATFWWVS GLVWRGYRRP LRPKDLWSLG
241  RENSSEELVS RLEKEWMRNR SAARRHNKAI AFKRKGGSGM KAPETEPFLR QEGSQWRPLL
301  KAIWQVFHST FLLGTLSLII SDVFRFTVPK LLSLFLEFIG DPKPPAWKGY LLAVLMFLSA
361  CLQTLFEQQN MYRLKVPQMR LRSAITGLVY RKVLALSSGS RKASAVGDVV NLVSVDVQRL
421  TESVLYLNGL WLPLVWIVVC FVYLWQLLGP SALTAIAVFL SLLPLNFFIS KKRNHHQEEQ
481  MRQKDSRARL TSSILRNSKT IKFHGWEGAF LDRVLGIRGQ ELGALRTSGL LFSVSLVSFQ
541  VSTFLVALVV FAVHTLVAEN AMNAEKAFVT LTVLNILNKA QAFLPFSIHS LVQARVSFDR
                                                  NBF1
601  LVTFLCLEEV DPGVVDSSSS GSAAGKDCIT IHSATFAWSQ ESPPCLHRIN LTVPQGCLLA
661  VVGPVGAGKS SLLSALLGEL SKVEGFVSIE GAVAYVPQEA WVQNTSVVEN VCFGQELDPP
        A
721  WLERVLEACA LQPDVDSFPE GIHTSIGEQG MNLSGGQKQR LSLARAVYRK AAVYLLDDPL
                NBF1                            C                    B
781  AALDAHVGQH VFNQVIGPGG LLQGTTRILV THALHILPQA DWIIVLANGA IAEMGSYQEL
841  LQRKGALVCL LDQARQPGDR GEGETEPGTS TKDPRGTSAG RRPELRRERS IKSVPEKDRT
901  TSEAQTEVPL DDPDRAGWPA GKDSIQYGRV KATVHLAYLR AVGTPLCLYA LFLFLCQQVA
961  SFCRGYWLSL WADDPAVGGQ QTQAALRGGI FGLLGCLQAI GLFASMAAVL LGGARASRLL
1021 FQRLLWDVVR SPISFFERTP IGHLLNRFSK ETDTVDVDIP DKLRSLLMYA FGLLEVSLVV
1081 AVATPLATVA ILPLFLLYAG FQSLYVVSSC QLRRLESASY SSVCSHMAET FQGSTVVRAF
1141 RTQAPFVAQN NARVDESQRI SFPRLVADRW LAANVELLGN GLVFAAATCA VLSKAHLSAG
1201 LVGFSVSAAL QVTQALQWVV RNWTDLENSI VSVERMQDYA WTPKEAPWRL PTCAAQPPWP
                              NBF2
1261 QGGQIEFRDF GLRYRPELPL AVQGVSLKIH AGEKVGIVGR TGAGKSSLAS GLLRLQEAAE
                                                  A
1321 GGIWIDGVPI AHVGLHTLRS RISIIPQDPI LFPGSLRMNL DLLQEHSDEA IWAALETVQL
                                                                 NBF2
1381 KALVASLPGQ LQYKCADRGE DLSVGQKQLL CLARALLRKT QILILDEATA AVDPGTELQM
                                C                    B
1441 QAMLGSWFAQ CTVLLIAHRL RSVMDCARVL VMDKGQVAES GSPAQLLAQK GLFYRLAQES
1501 GLV
```

Figure 9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Hum/MOATB
Hum/MOATC
Hum/MOATD
Hum/MRP
Hum/cMOAT
Hum/MDR1
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200
400
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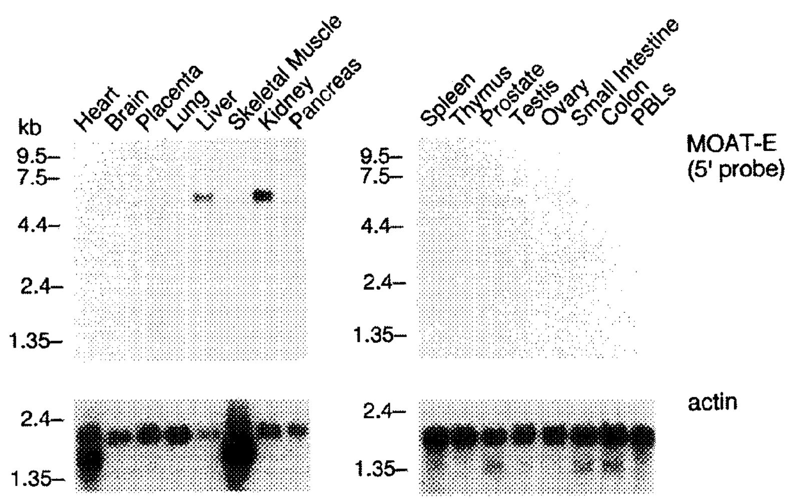
1000
1200
1400
1600

Figure 10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Heart
Brain
Placenta
Lung
Liver
Skeletal Muscle
Kidney
Pancreas
Spleen
Thymus
Prostate
Testis
Ovary
Small Intestine
Colon
PBLs
9.5–
7.5–
4.4–
2.4–
1.35–
MOAT-E
(5' probe)
actin

Figure 11

MOAT B cDNA AND AMINO ACID SEQUENCE ENCODED THEREBY

```
     ATGCTGCCCGTGTACCAGGAGGTGAAGCCCAACCCGCTGCAGGACGCGAACATCTGCTCA
   1 ---------+---------+---------+---------+---------+---------+ 60
     TACGACGGGCACATGGTCCTCCACTTCGGGTTGGGCGACGTCCTGCGCTTGTAGACGAGT

a    M  L  P  V  Y  Q  E  V  K  P  N  P  L  Q  D  A  N  I  C  S  -

     CGCGTGTTCTTCTGGTGGCTCAATCCCTTGTTTAAAATTGGCCATAAACGGAGATTAGAG
  61 ---------+---------+---------+---------+---------+---------+ 120
     GCGCACAAGAAGACCACCGAGTTAGGGAACAAATTTTAACCGGTATTTGCCTCTAATCTC

a    R  V  F  F  W  W  L  N  P  L  F  K  I  G  H  K  R  R  L  E  -

     GAAGATGATATGTATTCAGTGCTGCCAGAAGACCGCTCACAGCACCTTGGAGAGGAGTTG
 121 ---------+---------+---------+---------+---------+---------+ 180
     CTTCTACTATACATAAGTCACGACGGTCTTCTGGCGAGTGTCGTGGAACCTCTCCTCAAC

a    E  D  D  M  Y  S  V  L  P  E  D  R  S  Q  H  L  G  E  E  L  -

     CAAGGGTTCTGGGATAAAGAAGTTTTAAGAGCTGAGAATGACGCACAGAAGCCTTCTTTA
 181 ---------+---------+---------+---------+---------+---------+ 240
     GTTCCCAAGACCCTATTTCTTCAAAATTCTCGACTCTTACTGCGTGTCTTCGGAAGAAAT

a    Q  G  F  W  D  K  E  V  L  R  A  E  N  D  A  Q  K  P  S  L  -

     ACAAGAGCAATCATAAAGTGTTACTGGAAATCTTATTTAGTTTTGGGAATTTTTACGTTA
 241 ---------+---------+---------+---------+---------+---------+ 300
     TGTTCTCGTTAGTATTTCACAATGACCTTTAGAATAAATCAAAACCCTTAAAAATGCAAT

a    T  R  A  I  I  K  C  Y  W  K  S  Y  L  V  L  G  I  F  T  L  -

     ATTGAGGAAAGTGCCAAAGTAATCCAGCCCATATTTTTGGGAAAAATTATTAATTATTTT
 301 ---------+---------+---------+---------+---------+---------+ 360
     TAACTCCTTTCACGGTTTCATTAGGTCGGGTATAAAAACCCTTTTTAATAATTAATAAAA

a    I  E  E  S  A  K  V  I  Q  P  I  F  L  G  K  I  I  N  Y  F  -

     GAAAATTATGATCCCATGGATTCTGTGGCTTTGAACACAGCGTACGCCTATGCCACGGTG
```

Figure 12A

```
361 ---------+---------+---------+---------+---------+---------+ 420
    CTTTTAATACTAGGGTACCTAAGACACCGAAACTTGTGTCGCATGCGGATACGGTGCCAC

a   E N Y D P M D S V A L N T A Y A Y A T V -

    CTGACTTTTTGCACGCTCATTTTGGCTATACTGCATCACTTATATTTTTATCACGTTCAG
421 ---------+---------+---------+---------+---------+---------+ 480
    GACTGAAAAACGTGCGAGTAAAACCGATATGACGTAGTGAATATAAAAATAGTGCAAGTC

a   L T F C T L I L A I L H H L Y F Y H V Q -

    TGTGCTGGGATGAGGTTACGAGTAGCCATGTGCCATATGATTTATCGGAAGGCACTTCGT
481 ---------+---------+---------+---------+---------+---------+ 540
    ACACGACCCTACTCCAATGCTCATCGGTACACGGTATACTAAATAGCCTTCCGTGAAGCA

a   C A G M R L R V A M C H M I Y R K A L R -

    CTTAGTAACATGGCCATGGGGAAGACAACCACAGGCCAGATAGTCAATCTGCTGTCCAAT
541 ---------+---------+---------+---------+---------+---------+ 600
    GAATCATTGTACCGGTACCCCTTCTGTTGGTGTCCGGTCTATCAGTTAGACGACAGGTTA

a   L S N M A M G K T T T G Q I V N L L S N -

    GATGTGAACAAGTTTGATCAGGTGACAGTGTTCTTACACTTCCTGTGGGCAGGACCACTG
601 ---------+---------+---------+---------+---------+---------+ 660
    CTACACTTGTTCAAACTAGTCCACTGTCACAAGAATGTGAAGGACACCCGTCCTGGTGAC

a   D V N K F D Q V T V F L H F L W A G P L -

    CAGGCGATCGCAGTGACTGCCCTACTCTGGATGGAGATAGGAATATCGTGCCTTGCTGGG
661 ---------+---------+---------+---------+---------+---------+ 720
    GTCCGCTAGCGTCACTGACGGGATGAGACCTACCTCTATCCTTATAGCACGGAACGACCC

a   Q A I A V T A L L W M E I G I S C L A G -

    ATGGCAGTTCTAATCATTCTCCTGCCCTTGCAAAGCTGTTTTGGGAAGTTGTTCTCATCA
721 ---------+---------+---------+---------+---------+---------+ 780
    TACCGTCAAGATTAGTAAGAGGACGGGAACGTTTCGACAAAACCCTTCAACAAGAGTAGT

a   M A V L I I L L P L Q S C F G K L F S S -

    CTGAGGAGTAAAACTGCAACTTTCACGGATGCCAGGATCAGGACCATGAATGAAGTTATA
781 ---------+---------+---------+---------+---------+---------+ 840
```

Figure 12B

GACTCCTCATTTTGACGTTGAAAGTGCCTACGGTCCTAGTCCTGGTACTTACTTCAATAT

a L R S K T A T F T D A R I R T M N E V I -

ACTGGTATAAGGATAATAAAAATGTACGCCTGGGAAAAGTCATTTTCAAATCTTATTACC
841 ---------+---------+---------+---------+---------+---------+ 900
TGACCATATTCCTATTATTTTTACATGCGGACCCTTTTCAGTAAAAGTTTAGAATAATGG

a T G I R I I K M Y A W E K S F S N L I T -

AATTTGAGAAAGAAGGAGATTTCCAAGATTCTGAGAAGTTCCTGCCTCAGGGGGATGAAT
901 ---------+---------+---------+---------+---------+---------+ 960
TTAAACTCTTTCTTCCTCTAAAGGTTCTAAGACTCTTCAAGGACGGAGTCCCCCTACTTA

a N L R K K E I S K I L R S S C L R G M N -

TTGGCTTCGTTTTTCAGTGCAAGCAAAATCATCGTGTTTGTGACCTTCACCACCTACGTG
961 ---------+---------+---------+---------+---------+---------+ 1020
AACCGAAGCAAAAAGTCACGTTCGTTTTAGTAGCACAAACACTGGAAGTGGTGGATGCAC

a L A S F F S A S K I I V F V T F T T Y V -

CTCCTCGGCAGTGTGATCACAGCCAGCCGCGTGTTCGTGGCAGTGACGCTGTATGGGGCT
1021 ---------+---------+---------+---------+---------+---------+ 1080
GAGGAGCCGTCACACTAGTGTCGGTCGGCGCACAAGCACCGTCACTGCGACATACCCCGA

a L L G S V I T A S R V F V A V T L Y G A -

GTGCGGCTGACGGTTACCCTCTTCTTCCCCTCAGCCATTGAGAGGGTGTCAGAGGCAATC
1081 ---------+---------+---------+---------+---------+---------+ 1140
CACGCCGACTGCCAATGGGAGAAGAAGGGGAGTCGGTAACTCTCCCACAGTCTCCGTTAG

a V R L T V T L F F P S A I E R V S E A I -

GTCAGCATCCGAAGAATCCAGACCTTTTTGCTACTTGATGAGATATCACAGCGCAACCGT
1141 ---------+---------+---------+---------+---------+---------+ 1200
CAGTCGTAGGCTTCTTAGGTCTGGAAAAACGATGAACTACTCTATAGTGTCGCGTTGGCA

a V S I R R I Q T F L L L D E I S Q R N R -

CAGCTGCCGTCAGATGGTAAAAAGATGGTGCATGTGCAGGATTTTACTGCTTTTTGGGAT
1201 ---------+---------+---------+---------+---------+---------+ 1260
GTCGACGGCAGTCTACCATTTTTCTACCACGTACACGTCCTAAAATGACGAAAAACCCTA

Figure 12C

```
a     Q L P S D G K K M V H V Q D F T A F W D -

      AAGGCATCAGAGACCCCAACTCTACAAGGCCTTTCCTTTACTGTCAGACCTGGCGAATTG
 1261 ---------+---------+---------+---------+---------+---------+ 1320
      TTCCGTAGTCTCTGGGGTTGAGATGTTCCGGAAAGGAAATGACAGTCTGGACCGCTTAAC

a     K A S E T P T L Q G L S F T V R P G E L -

      TTAGCTGTGGTCGGCCCCGTGGGAGCAGGGAAGTCATCACTGTTAAGTGCCGTGCTCGGG
 1321 ---------+---------+---------+---------+---------+---------+ 1380
      AATCGACACCAGCCGGGGCACCCTCGTCCCTTCAGTAGTGACAATTCACGGCACGAGCCC

a     L A V V G P V G A G K S S L L S A V L G -

      GAATTGGCCCCAAGTCACGGGCTGGTCAGCGTGCATGGAAGAATTGCCTATGTGTCTCAG
 1381 ---------+---------+---------+---------+---------+---------+ 1440
      CTTAACCGGGGTTCAGTGCCCGACCAGTCGCACGTACCTTCTTAACGGATACACAGAGTC

a     E L A P S H G L V S V H G R I A Y V S Q -

      CAGCCCTGGGTGTTCTCGGGAACTCTGAGGAGTAATATTTTATTTGGGAAGAAATATGAA
 1441 ---------+---------+---------+---------+---------+---------+ 1500
      GTCGGGACCCACAAGAGCCCTTGAGACTCCTCATTATAAAATAAACCCTTCTTTATACTT

a     Q P W V F S G T L R S N I L F G K K Y E -

      AAGGAACGATATGAAAAAGTCATAAAGGCTTGTGCTCTGAAAAAGGATTTACAGCTGTTG
 1501 ---------+---------+---------+---------+---------+---------+ 1560
      TTCCTTGCTATACTTTTTCAGTATTTCCGAACACGAGACTTTTTCCTAAATGTCGACAAC

a     K E R Y E K V I K A C A L K K D L Q L L -

      GAGGATGGTGATCTGACTGTGATAGGAGATCGGGGAACCACGCTGAGTGGAGGGCAGAAA
 1561 ---------+---------+---------+---------+---------+---------+ 1620
      CTCCTACCACTAGACTGACACTATCCTCTAGCCCCTTGGTGCGACTCACCTCCCGTCTTT

a     E D G D L T V I G D R G T T L S G G Q K -

      GCACGGGTAAACCTTGCAAGAGCAGTGTATCAAGATGCTGACATCTATCTCCTGGACGAT
 1621 ---------+---------+---------+---------+---------+---------+ 1680
      CGTGCCCATTTGGAACGTTCTCGTCACATAGTTCTACGACTGTAGATAGAGGACCTGCTA
```

Figure 12D

```
a     A R V N L A R A V Y Q D A D I Y L L D D -

      CCTCTCAGTGCAGTAGATGCGGAAGTTAGCAGACACTTGTTCGAACTGTGTATTTGTCAA
 1681 ---------+---------+---------+---------+---------+---------+ 1740
      GGAGAGTCACGTCATCTACGCCTTCAATCGTCTGTGAACAAGCTTGACACATAAACAGTT

a     P L S A V D A E V S R H L F E L C I C Q -

      ATTTTGCATGAGAAGATCACAATTTTAGTGACTCATCAGTTGCAGTACCTCAAAGCTGCA
 1741 ---------+---------+---------+---------+---------+---------+ 1800
      TAAAACGTACTCTTCTAGTGTTAAAATCACTGAGTAGTCAACGTCATGGAGTTTCGACGT

a     I L H E K I T I L V T H Q L Q Y L K A A -

      AGTCAGATTCTGATATTGAAAGATGGTAAAATGGTGCAGAAGGGGACTTACACTGAGTTC
 1801 ---------+---------+---------+---------+---------+---------+ 1860
      TCAGTCTAAGACTATAACTTTCTACCATTTTACCACGTCTTCCCCTGAATGTGACTCAAG

a     S Q I L I L K D G K M V Q K G T Y T E F -

      CTAAAATCTGGTATAGATTTTGGCTCCCTTTTAAAGAAGGATAATGAGGAAAGTGAACAA
 1861 ---------+---------+---------+---------+---------+---------+ 1920
      GATTTTAGACCATATCTAAAACCGAGGGAAAATTTCTTCCTATTACTCCTTTCACTTGTT

a     L K S G I D F G S L L K K D N E E S E Q -

      CCTCCAGTTCCAGGAACTCCCACACTAAGGAATCGTACCTTCTCAGAGTCTTCGGTTTGG
 1921 ---------+---------+---------+---------+---------+---------+ 1980
      GGAGGTCAAGGTCCTTGAGGGTGTGATTCCTTAGCATGGAAGAGTCTCAGAAGCCAAACC

a     P P V P G T P T L R N R T F S E S S V W -

      TCTCAACAATCTTCTAGACCCTCCTTGAAAGATGGTGCTCTGGAGAGCCAAGATACAGAG
 1981 ---------+---------+---------+---------+---------+---------+ 2040
      AGAGTTGTTAGAAGATCTGGGAGGAACTTTCTACCACGAGACCTCTCGGTTCTATGTCTC

a     S Q Q S S R P S L K D G A L E S Q D T E -

      AATGTCCCAGTTACACTATCAGAGGAGAACCGTTCTGAAGGAAAAGTTGGTTTTCAGGCC
 2041 ---------+---------+---------+---------+---------+---------+ 2100
      TTACAGGGTCAATGTGATAGTCTCCTCTTGGCAAGACTTCCTTTTCAACCAAAAGTCCGG

a     N V P V T L S E E N R S E G K V G F Q A
```

Figure 12E

```
     TATAAGAATTACTTCAGAGCTGGTGCTCACTGGATTGTCTTCATTTTCCTTATTCTCCTA
2101 ---------+---------+---------+---------+---------+---------+ 2160
     ATATTCTTAATGAAGTCTCGACCACGAGTGACCTAACAGAAGTAAAAGGAATAAGAGGAT

a     Y  K  N  Y  F  R  A  G  A  H  W  I  V  F  I  F  L  I  L  L  -

     AACACTGCAGCTCAGGTTGCCTATGTGCTTCAAGATTGGTGGCTTTCATACTGGGCAAAC
2161 ---------+---------+---------+---------+---------+---------+ 2220
     TTGTGACGTCGAGTCCAACGGATACACGAAGTTCTAACCACCGAAAGTATGACCCGTTTG

a     N  T  A  A  Q  V  A  Y  V  L  Q  D  W  W  L  S  Y  W  A  N  -

     AAACAAAGTATGCTAAATGTCACTGTAAATGGAGGAGGAAATGTAACCGAGAAGCTAGAT
2221 ---------+---------+---------+---------+---------+---------+ 2280
     TTTGTTTCATACGATTTACAGTGACATTTACCTCCTCCTTTACATTGGCTCTTCGATCTA

a     K  Q  S  M  L  N  V  T  V  N  G  G  G  N  V  T  E  K  L  D  -

     CTTAACTGGTACTTAGGAATTTATTCAGGTTTAACTGTAGCTACCGTTCTTTTTGGCATA
2281 ---------+---------+---------+---------+---------+---------+ 2340
     GAATTGACCATGAATCCTTAAATAAGTCCAAATTGACATCGATGGCAAGAAAAACCGTAT

a     L  N  W  Y  L  G  I  Y  S  G  L  T  V  A  T  V  L  F  G  I  -

     GCAAGATCTCTATTGGTATTCTACGTCCTTGTTAACTCTTCACAAACTTTGCACAACAAA
2341 ---------+---------+---------+---------+---------+---------+ 2400
     CGTTCTAGAGATAACCATAAGATGCAGGAACAATTGAGAAGTGTTTGAAACGTGTTGTTT

a     A  R  S  L  L  V  F  Y  V  L  V  N  S  S  Q  T  L  H  N  K  -

     ATGTTTGAGTCAATTCTGAAAGCTCCGGTATTATTCTTTGATAGAAATCCAATAGGAAGA
2401 ---------+---------+---------+---------+---------+---------+ 2460
     TACAAACTCAGTTAAGACTTTCGAGGCCATAATAAGAAACTATCTTTAGGTTATCCTTCT

a     M  F  E  S  I  L  K  A  P  V  L  F  F  D  R  N  P  I  G  R  -

     ATTTTAAATCGTTTCTCCAAAGACATTGGACACTTGGATGATTTGCTGCCGCTGACGTTT
2461 ---------+---------+---------+---------+---------+---------+ 2520
     TAAAATTTAGCAAAGAGGTTTCTGTAACCTGTGAACCTACTAAACGACGGCGACTGCAAA

a     I  L  N  R  F  S  K  D  I  G  H  L  D  D  L  L  P  L  T  F
```

Figure 12F

```
     TTAGATTTCATCCAGACATTGCTACAAGTGGTTGGTGTGGTCTCTGTGGCTGTGGCCGTG
2521 ---------+---------+---------+---------+---------+---------+ 2580
     AATCTAAAGTAGGTCTGTAACGATGTTCACCAACCACACCAGAGACACCGACACCGGCAC

a    L D F I Q T L L Q V V G V V S V A V A V -

     ATTCCTTGGATCGCAATACCCTTGGTTCCCCTTGGAATCATTTTCATTTTTCTTCGGCGA
2581 ---------+---------+---------+---------+---------+---------+ 2640
     TAAGGAACCTAGCGTTATGGGAACCAAGGGGAACCTTAGTAAAAGTAAAAAGAAGCCGCT

a    I P W I A I P L V P L G I I F I F L R R -

     TATTTTTTGGAAACGTCAAGAGATGTGAAGCGCCTGGAATCTACAACTCGGAGTCCAGTG
2641 ---------+---------+---------+---------+---------+---------+ 2700
     ATAAAAAACCTTTGCAGTTCTCTACACTTCGCGGACCTTAGATGTTGAGCCTCAGGTCAC

a    Y F L E T S R D V K R L E S T T R S P V -

     TTTTCCCACTTGTCATCTTCTCTCCAGGGGCTCTGGACCATCCGGGCATACAAAGCAGAA
2701 ---------+---------+---------+---------+---------+---------+ 2760
     AAAAGGGTGAACAGTAGAAGAGAGGTCCCCGAGACCTGGTAGGCCCGTATGTTTCGTCTT

a    F S H L S S S L Q G L W T I R A Y K A E -

     GAGAGGTGTCAGGAACTGTTTGATGCACACCAGGATTTACATTCAGAGGCTTGGTTCTTG
2761 ---------+---------+---------+---------+---------+---------+ 2820
     CTCTCCACAGTCCTTGACAAACTACGTGTGGTCCTAAATGTAAGTCTCCGAACCAAGAAC

a    E R C Q E L F D A H Q D L H S E A W F L -

     TTTTTGACAACGTCCCGCTGGTTCGCCGTCCGTCTGGATGCCATCTGTGCCATGTTTGTC
2821 ---------+---------+---------+---------+---------+---------+ 2880
     AAAAACTGTTGCAGGGCGACCAAGCGGCAGGCAGACCTACGGTAGACACGGTACAAACAG

a    F L T T S R W F A V R L D A I C A M F V -

     ATCATCGTTGCCTTTGGGTCCCTGATTCTGGCAAAAACTCTGGATGCCGGGCAGGTTGGT
2881 ---------+---------+---------+---------+---------+---------+ 2940
     TAGTAGCAACGGAAACCCAGGGACTAAGACCGTTTTTGAGACCTACGGCCCGTCCAACCA

a    I I V A F G S L I L A K T L D A G Q V G -

     TTGGCACTGTCCTATGCCCTCACGCTCATGGGGATGTTTCAGTGGTGTGTTCGACAAAGT
```

Figure 12G

SUBSTITUTE SHEET (RULE 26)

```
2941 ---------+---------+---------+---------+---------+---------+ 3000
     AACCGTGACAGGATACGGGAGTGCGAGTACCCCTACAAAGTCACCACACAAGCTGTTTCA

a    L A L S Y A L T L M G M F Q W C V R Q S -

     GCTGAAGTTGAGAATATGATGATCTCAGTAGAAAGGGTCATTGAATACACAGACCTTGAA
3001 ---------+---------+---------+---------+---------+---------+ 3060
     CGACTTCAACTCTTATACTACTAGAGTCATCTTTCCCAGTAACTTATGTGTCTGGAACTT

a    A E V E N M M I S V E R V I E Y T D L E -

     AAAGAAGCACCTTGGGAATATCAGAAACGCCCACCACCAGCCTGGCCCCATGAAGGAGTG
3061 ---------+---------+---------+---------+---------+---------+ 3120
     TTTCTTCGTGGAACCCTTATAGTCTTTGCGGGTGGTGGTCGGACCGGGGTACTTCCTCAC

a    K E A P W E Y Q K R P P P A W P H E G V -

     ATAATCTTTGACAATGTGAACTTCATGTACAGTCCAGGTGGGCCTCTGGTACTGAAGCAT
3121 ---------+---------+---------+---------+---------+---------+ 3180
     TATTAGAAACTGTTACACTTGAAGTACATGTCAGGTCCACCCGGAGACCATGACTTCGTA

a    I I F D N V N F M Y S P G G P L V L K H -

     CTGACAGCACTCATTAAATCACAAGAAAAGGTTGGCATTGTGGGAAGAACCGGAGCTGGA
3181 ---------+---------+---------+---------+---------+---------+ 3240
     GACTGTCGTGAGTAATTTAGTGTTCTTTTCCAACCGTAACACCCTTCTTGGCCTCGACCT

a    L T A L I K S Q E K V G I V G R T G A G -

     AAAAGTTCCCTCATCTCAGCCCTTTTTAGATTGTCAGAACCCGAAGGTAAAATTTGGATT
3241 ---------+---------+---------+---------+---------+---------+ 3300
     TTTTCAAGGGAGTAGAGTCGGGAAAAATCTAACAGTCTTGGGCTTCCATTTTAAACCTAA

a    K S S L I S A L F R L S E P E G K I W I -

     GATAAGATCTTGACAACTGAAATTGGACTTCACGATTTAAGGAAGAAAATGTCAATCATA
3301 ---------+---------+---------+---------+---------+---------+ 3360
     CTATTCTAGAACTGTTGACTTTAACCTGAAGTGCTAAATTCCTTCTTTTACAGTTAGTAT

a    D K I L T T E I G L H D L R K K M S I I -

     CCTCAGGAACCTGTTTTGTTCACTGGAACAATGAGGAAAAACCTGGATCCCTTTAAGGAG
3361 ---------+---------+---------+---------+---------+---------+ 3420
```

Figure 12H

SUBSTITUTE SHEET (RULE 26)

```
      GGAGTCCTTGGACAAAACAAGTGACCTTGTTACTCCTTTTTGGACCTAGGGAAATTCCTC

a     P  Q  E  P  V  L  F  T  G  T  M  R  K  N  L  D  P  F  K  E  -

      CACACGGATGAGGAACTGTGGAATGCCTTACAAGAGGTACAACTTAAAGAAACCATTGAA
 3421 ---------+---------+---------+---------+---------+---------+   3480
      GTGTGCCTACTCCTTGACACCTTACGGAATGTTCTCCATGTTGAATTTCTTTGGTAACTT

a     H  T  D  E  E  L  W  N  A  L  Q  E  V  Q  L  K  E  T  I  E  -

      GATCTTCCTGGTAAAATGGATACTGAATTAGCAGAATCAGGATCCAATTTTAGTGTTGGA
 3481 ---------+---------+---------+---------+---------+---------+   3540
      CTAGAAGGACCATTTTACCTATGACTTAATCGTCTTAGTCCTAGGTTAAAATCACAACCT

a     D  L  P  G  K  M  D  T  E  L  A  E  S  G  S  N  F  S  V  G  -

      CAAAGACAACTGGTGTGCCTTGCCAGGGCAATTCTCAGGAAAAATCAGATATTGATTATT
 3541 ---------+---------+---------+---------+---------+---------+   3600
      GTTTCTGTTGACCACACGGAACGGTCCCGTTAAGAGTCCTTTTTAGTCTATAACTAATAA

a     Q  R  Q  L  V  C  L  A  R  A  I  L  R  K  N  Q  I  L  I  I  -

      GATGAAGCGACGGCAAATGTGGATCCAAGAACTGATGAGTTAATACAAAAAAAAATCCGG
 3601 ---------+---------+---------+---------+---------+---------+   3660
      CTACTTCGCTGCCGTTTACACCTAGGTTCTTGACTACTCAATTATGTTTTTTTTTAGGCC

a     D  E  A  T  A  N  V  D  P  R  T  D  E  L  I  Q  K  K  I  R  -

      GAGAAATTTGCCCACTGCACCGTGCTAACCATTGCACACAGATTGAACACCATTATTGAC
 3661 ---------+---------+---------+---------+---------+---------+   3720
      CTCTTTAAACGGGTGACGTGGCACGATTGGTAACGTGTGTCTAACTTGTGGTAATAACTG

a     E  K  F  A  H  C  T  V  L  T  I  A  H  R  L  N  T  I  I  D  -

      AGCGACAAGATAATGGTTTTAGATTCAGGAAGACTGAAAGAATATGATGAGCCGTATGTT
 3721 ---------+---------+---------+---------+---------+---------+   3780
      TCGCTGTTCTATTACCAAAATCTAAGTCCTTCTGACTTTCTTATACTACTCGGCATACAA

a     S  D  K  I  M  V  L  D  S  G  R  L  K  E  Y  D  E  P  Y  V  -

      TTGCTGCAAAATAAAGAGAGCCTATTTTACAAGATGGTGCAACAACTGGGCAAGGCAGAA
 3781 ---------+---------+---------+---------+---------+---------+   3840
      AACGACGTTTTATTTCTCTCGGATAAAATGTTCTACCACGTTGTTGACCCGTTCCGTCTT
```

Figure 12I

```
a     L  L  Q  N  K  E  S  L  F  Y  K  M  V  Q  Q  L  G  K  A  E  -

      GCCGCTGCCCTCACTGAAACAGCAAAACAGGTATACTTCAAAAGAAATTATCCACATATT
 3841 ---------+---------+---------+---------+---------+---------+  3900
      CGGCGACGGGAGTGACTTTGTCGTTTTGTCCATATGAAGTTTTCTTTAATAGGTGTATAA

a     A  A  A  L  T  E  T  A  K  Q  V  Y  F  K  R  N  Y  P  H  I  -

      GGTCACACTGACCACATGGTTACAAACACTTCCAATGGACAGCCCTCGACCTTAACTATT
 3901 ---------+---------+---------+---------+---------+---------+  3960
      CCAGTGTGACTGGTGTACCAATGTTTGTGAAGGTTACCTGTCGGGAGCTGGAATTGATAA

a     G  H  T  D  H  M  V  T  N  T  S  N  G  Q  P  S  T  L  T  I  -

      TTCGAGACAGCACTG
 3961 ---------+-----  3975
      AAGCTCTGTCGTGAC

a     F  E  T  A  L  -
```

Figure 12J

SUBSTITUTE SHEET (RULE 26)

MOAT C cDNA AND AMINO ACID SEQUENCE ENCODED THEREBY

```
    ATGAAGGATATCGACATAGGAAAAGAGTATATCATCCCCAGTCCTGGGTATAGAAGTGTG
  1 ---------+---------+---------+---------+---------+---------+ 60
    TACTTCCTATAGCTGTATCCTTTTCTCATATAGTAGGGGTCAGGACCCATATCTTCACAC

a    M  K  D  I  D  I  G  K  E  Y  I  I  P  S  P  G  Y  R  S  V  -

    AGGGAGAGAACCAGCACTTCTGGGACGCACAGAGACCGTGAAGATTCCAAGTTCAGGAGA
 61 ---------+---------+---------+---------+---------+---------+ 120
    TCCCTCTCTTGGTCGTGAAGACCCTGCGTGTCTCTGGCACTTCTAAGGTTCAAGTCCTCT

a    R  E  R  T  S  T  S  G  T  H  R  D  R  E  D  S  K  F  R  R  -

    ACTCGACCGTTGGAATGCCAAGATGCCTTGGAAACAGCAGCCCGAGCCGAGGGCCTCTCT
121 ---------+---------+---------+---------+---------+---------+ 180
    TGAGCTGGCAACCTTACGGTTCTACGGAACCTTTGTCGTCGGGCTCGGCTCCCGGAGAGA

a    T  R  P  L  E  C  Q  D  A  L  E  T  A  A  R  A  E  G  L  S  -

    CTTGATGCCTCCATGCATTCTCAGCTCAGAATCCTGGATGAGGAGCATCCCAAGGGAAAG
181 ---------+---------+---------+---------+---------+---------+ 240
    GAACTACGGAGGTACGTAAGAGTCGAGTCTTAGGACCTACTCCTCGTAGGGTTCCCTTTC

a    L  D  A  S  M  H  S  Q  L  R  I  L  D  E  E  H  P  K  G  K  -

    TACCATCATGGCTTGAGTGCTCTGAAGCCCATCCGGACTACTTCCAAACACCAGCACCCA
241 ---------+---------+---------+---------+---------+---------+ 300
    ATGGTAGTACCGAACTCACGAGACTTCGGGTAGGCCTGATGAAGGTTTGTGGTCGTGGGT

a    Y  H  H  G  L  S  A  L  K  P  I  R  T  T  S  K  H  Q  H  P  -

    GTGGACAATGCTGGGCTTTTTTCCTGTATGACTTTTTCGTGGCTTTCTTCTCTGGCCCGT
301 ---------+---------+---------+---------+---------+---------+ 360
    CACCTGTTACGACCCGAAAAAAGGACATACTGAAAAAGCACCGAAAGAAGAGACCGGGCA

a    V  D  N  A  G  L  F  S  C  M  T  F  S  W  L  S  S  L  A  R  -

    GTGGCCCACAAGAAGGGGGAGCTCTCAATGGAAGACGTGTGGTCTCTGTCCAAGCACGAG
```

Figure 13A

```
361 ---------+---------+---------+---------+---------+---------+ 420
    CACCGGGTGTTCTTCCCCCTCGAGAGTTACCTTCTGCACACCAGAGACAGGTTCGTGCTC

a   V  A  H  K  K  G  E  L  S  M  E  D  V  W  S  L  S  K  H  E  -

    TCTTCTGACGTGAACTGCAGAAGACTAGAGAGACTGTGGCAAGAAGAGCTGAATGAAGTT
421 ---------+---------+---------+---------+---------+---------+ 480
    AGAAGACTGCACTTGACGTCTTCTGATCTCTCTGACACCGTTCTTCTCGACTTACTTCAA

a   S  S  D  V  N  C  R  R  L  E  R  L  W  Q  E  E  L  N  E  V  -

    GGGCCAGACGCTGCTTCCCTGCGAAGGGTTGTGTGGATCTTCTGCCGCACCAGGCTCATC
481 ---------+---------+---------+---------+---------+---------+ 540
    CCCGGTCTGCGACGAAGGGACGCTTCCCAACACACCTAGAAGACGGCGTGGTCCGAGTAG

a   G  P  D  A  A  S  L  R  R  V  V  W  I  F  C  R  T  R  L  I  -

    CTGTCCATCGTGTGCCTGATGATCACGCAGCTGGCTGGCTTCAGTGGACCAGCCTTCATG
541 ---------+---------+---------+---------+---------+---------+ 600
    GACAGGTAGCACACGGACTACTAGTGCGTCGACCGACCGAAGTCACCTGGTCGGAAGTAC

a   L  S  I  V  C  L  M  I  T  Q  L  A  G  F  S  G  P  A  F  M  -

    GTGAAACACCTCTTGGAGTATACCCAGGCAACAGAGTCTAACCTGCAGTACAGCTTGTTG
601 ---------+---------+---------+---------+---------+---------+ 660
    CACTTTGTGGAGAACCTCATATGGGTCCGTTGTCTCAGATTGGACGTCATGTCGAACAAC

a   V  K  H  L  L  E  Y  T  Q  A  T  E  S  N  L  Q  Y  S  L  L  -

    TTAGTGCTGGGCCTCCTCCTGACGGAAATCGTGCGGTCTTGGTCGCTTGCACTGACTTGG
661 ---------+---------+---------+---------+---------+---------+ 720
    AATCACGACCCGGAGGAGGACTGCCTTTAGCACGCCAGAACCAGCGAACGTGACTGAACC

a   L  V  L  G  L  L  L  T  E  I  V  R  S  W  S  L  A  L  T  W  -

    GCATTGAATTACCGAACCGGTGTCCGCTTGCGGGGGGCCATCCTAACCATGGCATTTAAG
721 ---------+---------+---------+---------+---------+---------+ 780
    CGTAACTTAATGGCTTGGCCACAGGCGAACGCCCCCCGGTAGGATTGGTACCGTAAATTC

a   A  L  N  Y  R  T  G  V  R  L  R  G  A  I  L  T  M  A  F  K  -

    AAGATCCTTAAGTTAAAGAACATTAAAGAGAAATCCCTGGGTGAGCTCATCAACATTTGC
781 ---------+---------+---------+---------+---------+---------+ 840
```

Figure 13B

```
     TTCTAGGAATTCAATTTCTTGTAATTTCTCTTTAGGGACCCACTCGAGTAGTTGTAAACG

a    K  I  L  K  L  K  N  I  K  E  K  S  L  G  E  L  I  N  I  C  -

     TCCAACGATGGGCAGAGAATGTTTGAGGCAGCAGCCGTTGGCAGCCTGCTGGCTGGAGGA
 841 ---------+---------+---------+---------+---------+---------+ 900
     AGGTTGCTACCCGTCTCTTACAAACTCCGTCGTCGGCAACCGTCGGACGACCGACCTCCT

a    S  N  D  G  Q  R  M  F  E  A  A  A  V  G  S  L  L  A  G  G  -

     CCCGTTGTTGCCATCTTAGGCATGATTTATAATGTAATTATTCTGGGACCAACAGGCTTC
 901 ---------+---------+---------+---------+---------+---------+ 960
     GGGCAACAACGGTAGAATCCGTACTAAATATTACATTAATAAGACCCTGGTTGTCCGAAG

a    P  V  V  A  I  L  G  M  I  Y  N  V  I  I  L  G  P  T  G  F  -

     CTGGGATCAGCTGTTTTTATCCTCTTTTACCCAGCAATGATGTTTGCATCACGGCTCACA
 961 ---------+---------+---------+---------+---------+---------+ 1020
     GACCCTAGTCGACAAAAATAGGAGAAAATGGGTCGTTACTACAAACGTAGTGCCGAGTGT

a    L  G  S  A  V  F  I  L  F  Y  P  A  M  M  F  A  S  R  L  T  -

     GCATATTTCAGGAGAAAATGCGTGGCCGCCACGGATGAACGTGTCCAGAAGATGAATGAA
1021 ---------+---------+---------+---------+---------+---------+ 1080
     CGTATAAAGTCCTCTTTTACGCACCGGCGGTGCCTACTTGCACAGGTCTTCTACTTACTT

a    A  Y  F  R  R  K  C  V  A  A  T  D  E  R  V  Q  K  M  N  E  -

     GTTCTTACTTACATTAAATTTATCAAAATGTATGCCTGGGTCAAAGCATTTTCTCAGAGT
1081 ---------+---------+---------+---------+---------+---------+ 1140
     CAAGAATGAATGTAATTTAAATAGTTTTACATACGGACCCAGTTTCGTAAAAGAGTCTCA

a    V  L  T  Y  I  K  F  I  K  M  Y  A  W  V  K  A  F  S  Q  S  -

     GTTCAGAAAATCCGCGAGGAGGAGCGTCGGATATTGGAAAAAGCCGGGTACTTCCAGGGT
1141 ---------+---------+---------+---------+---------+---------+ 1200
     CAAGTCTTTTAGGCGCTCCTCCTCGCAGCCTATAACCTTTTTCGGCCCATGAAGGTCCCA

a    V  Q  K  I  R  E  E  E  R  R  I  L  E  K  A  G  Y  F  Q  G  -

     ATCACTGTGGGTGTGGCTCCCATTGTGGTGGTGATTGCCAGCGTGGTGACCTTCTCTGTT
1201 ---------+---------+---------+---------+---------+---------+ 1260
     TAGTGACACCCACACCGAGGGTAACACCACCACTAACGGTCGCACCACTGGAAGAGACAA
```

Figure 13C

```
a    I  T  V  G  V  A  P  I  V  V  V  I  A  S  V  V  T  F  S  V  -

     CATATGACCCTGGGCTTCGATCTGACAGCAGCACAGGCTTTCACAGTGGTGACAGTCTTC
1261 ---------+---------+---------+---------+---------+---------+ 1320
     GTATACTGGGACCCGAAGCTAGACTGTCGTCGTGTCCGAAAGTGTCACCACTGTCAGAAG

a    H  M  T  L  G  F  D  L  T  A  A  Q  A  F  T  V  V  T  V  F  -

     AATTCCATGACTTTTGCTTTGAAAGTAACACCGTTTTCAGTAAAGTCCCTCTCAGAAGCC
1321 ---------+---------+---------+---------+---------+---------+ 1380
     TTAAGGTACTGAAAACGAAACTTTCATTGTGGCAAAAGTCATTTCAGGGAGAGTCTTCGG

a    N  S  M  T  F  A  L  K  V  T  P  F  S  V  K  S  L  S  E  A  -

     TCAGTGGCTGTTGACAGATTTAAGAGTTTGTTTCTAATGGAAGAGGTTCACATGATAAAG
1381 ---------+---------+---------+---------+---------+---------+ 1440
     AGTCACCGACAACTGTCTAAATTCTCAAACAAAGATTACCTTCTCCAAGTGTACTATTTC

a    S  V  A  V  D  R  F  K  S  L  F  L  M  E  E  V  H  M  I  K  -

     AACAAACCAGCCAGTCCTCACATCAAGATAGAGATGAAAAATGCCACCTTGGCATGGGAC
1441 ---------+---------+---------+---------+---------+---------+ 1500
     TTGTTTGGTCGGTCAGGAGTGTAGTTCTATCTCTACTTTTTACGGTGGAACCGTACCCTG

a    N  K  P  A  S  P  H  I  K  I  E  M  K  N  A  T  L  A  W  D  -

     TCCTCCCACTCCAGTATCCAGAACTCGCCCAAGCTGACCCCCAAAATGAAAAAAGACAAG
1501 ---------+---------+---------+---------+---------+---------+ 1560
     AGGAGGGTGAGGTCATAGGTCTTGAGCGGGTTCGACTGGGGGTTTTACTTTTTTCTGTTC

a    S  S  H  S  S  I  Q  N  S  P  K  L  T  P  K  M  K  K  D  K  -

     AGGGCTTCCAGGGGCAAGAAAGAGAAGGTGAGGCAGCTGCAGCGCACTGAGCATCAGGCG
1561 ---------+---------+---------+---------+---------+---------+ 1620
     TCCCGAAGGTCCCCGTTCTTTCTCTTCCACTCCGTCGACGTCGCGTGACTCGTAGTCCGC

a    R  A  S  R  G  K  K  E  K  V  R  Q  L  Q  R  T  E  H  Q  A  -

     GTGCTGGCAGAGCAGAAAGGCCACCTCCTCCTGGACAGTGACGAGCGGCCCAGTCCCGAA
1621 ---------+---------+---------+---------+---------+---------+ 1680
     CACGACCGTCTCGTCTTTCCGGTGGAGGAGGACCTGTCACTGCTCGCCGGGTCAGGGCTT
```

Figure 13D

```
a     V L A E Q K G H L L L D S D E R P S P E -

      GAGGAAGAAGGCAAGCACATCCACCTGGGCCACCTGCGCTTACAGAGGACACTGCACAGC
 1681 ---------+---------+---------+---------+---------+---------+  1740
      CTCCTTCTTCCGTTCGTGTAGGTGGACCCGGTGGACGCGAATGTCTCCTGTGACGTGTCG

a     E E E G K H I H L G H L R L Q R T L H S -

      ATCGATCTGGAGATCCAAGAGGGTAAACTGGTTGGAATCTGCGGCAGTGTGGGAAGTGGA
 1741 ---------+---------+---------+---------+---------+---------+  1800
      TAGCTAGACCTCTAGGTTCTCCCATTTGACCAACCTTAGACGCCGTCACACCCTTCACCT

a     I D L E I Q E G K L V G I C G S V G S G -

      AAAACCTCTCTCATTTCAGCCATTTTAGGCCAGATGACGCTTCTAGAGGGCAGCATTGCA
 1801 ---------+---------+---------+---------+---------+---------+  1860
      TTTTGGAGAGAGTAAAGTCGGTAAAATCCGGTCTACTGCGAAGATCTCCCGTCGTAACGT

a     K T S L I S A I L G Q M T L L E G S I A -

      ATCAGTGGAACCTTCGCTTATGTGGCCCAGCAGGCCTGGATCCTCAATGCTACTCTGAGA
 1861 ---------+---------+---------+---------+---------+---------+  1920
      TAGTCACCTTGGAAGCGAATACACCGGGTCGTCCGGACCTAGGAGTTACGATGAGACTCT

a     I S G T F A Y V A Q Q A W I L N A T L R -

      GACAACATCCTGTTTGGGAAGGAATATGATGAAGAAAGATACAACTCTGTGCTGAACAGC
 1921 ---------+---------+---------+---------+---------+---------+  1980
      CTGTTGTAGGACAAACCCTTCCTTATACTACTTCTTTCTATGTTGAGACACGACTTGTCG

a     D N I L F G K E Y D E E R Y N S V L N S -

      TGCTGCCTGAGGCCTGACCTGGCCATTCTTCCCAGCAGCGACCTGACGGAGATTGGAGAG
 1981 ---------+---------+---------+---------+---------+---------+  2040
      ACGACGGACTCCGGACTGGACCGGTAAGAAGGGTCGTCGCTGGACTGCCTCTAACCTCTC

a     C C L R P D L A I L P S S D L T E I G E -

      CGAGGAGCCAACCTGAGCGGTGGGCAGCGCCAGAGGATCAGCCTTGCCCGGGCCTTGTAT
 2041 ---------+---------+---------+---------+---------+---------+  2100
      GCTCCTCGGTTGGACTCGCCACCCGTCGCGGTCTCCTAGTCGGAACGGGCCCGGAACATA

a     R G A N L S G G Q R Q R I S L A R A L Y -
```

Figure 13E

```
     AGTGACAGGAGCATCTACATCCTGGACGACCCCCTCAGTGCCTTAGATGCCCATGTGGGC
2101 ---------+---------+---------+---------+---------+---------+ 2160
     TCACTGTCCTCGTAGATGTAGGACCTGCTGGGGGAGTCACGGAATCTACGGGTACACCCG

a    S D R S I Y I L D D P L S A L D A H V G -

     AACCACATCTTCAATAGTGCTATCCGGAAACATCTCAAGTCCAAGACAGTTCTGTTTGTT
2161 ---------+---------+---------+---------+---------+---------+ 2220
     TTGGTGTAGAAGTTATCACGATAGGCCTTTGTAGAGTTCAGGTTCTGTCAAGACAAACAA

a    N H I F N S A I R K H L K S K T V L F V -

     ACCCACCAGTTACAGTACCTGGTTGACTGTGATGAAGTGATCTTCATGAAAGAGGGCTGT
2221 ---------+---------+---------+---------+---------+---------+ 2280
     TGGGTGGTCAATGTCATGGACCAACTGACACTACTTCACTAGAAGTACTTTCTCCCGACA

a    T H Q L Q Y L V D C D E V I F M K E G C -

     ATTACGGAAAGAGGCACCCATGAGGAACTGATGAATTTAAATGGTGACTATGCTACCATT
2281 ---------+---------+---------+---------+---------+---------+ 2340
     TAATGCCTTTCTCCGTGGGTACTCCTTGACTACTTAAATTTACCACTGATACGATGGTAA

a    I T E R G T H E E L M N L N G D Y A T I -

     TTTAATAACCTGTTGCTGGGAGAGACACCGCCAGTTGAGATCAATTCAAAAAAGGAAACC
2341 ---------+---------+---------+---------+---------+---------+ 2400
     AAATTATTGGACAACGACCCTCTCTGTGGCGGTCAACTCTAGTTAAGTTTTTTCCTTTGG

a    F N N L L L G E T P P V E I N S K K E T -

     AGTGGTTCACAGAAGAAGTCACAAGACAAGGGTCCTAAAACAGGATCAGTAAAGAAGGAA
2401 ---------+---------+---------+---------+---------+---------+ 2460
     TCACCAAGTGTCTTCTTCAGTGTTCTGTTCCCAGGATTTTGTCCTAGTCATTTCTTCCTT

a    S G S Q K K S Q D K G P K T G S V K K E -

     AAAGCAGTAAAGCCAGAGGAAGGGCAGCTTGTGCAGCTGGAAGAGAAAGGGCAGGGTTCA
2461 ---------+---------+---------+---------+---------+---------+ 2520
     TTTCGTCATTTCGGTCTCCTTCCCGTCGAACACGTCGACCTTCTCTTTCCCGTCCCAAGT

a    K A V K P E E G Q L V Q L E E K G Q G S -
```

Figure 13F

SUBSTITUTE SHEET (RULE 26)

```
     GTGCCCTGGTCAGTATATGGTGTCTACATCCAGGCTGCTGGGGGCCCCTTGGCATTCCTG
2521 ---------+---------+---------+---------+---------+---------+ 2580
     CACGGGACCAGTCATATACCACAGATGTAGGTCCGACGACCCCCGGGGAACCGTAAGGAC

a    V P W S V Y G V Y I Q A A G G P L A F L -

     GTTATTATGGCCCTTTTCATGCTGAATGTAGGCAGCACCGCCTTCAGCACCTGGTGGTTG
2581 ---------+---------+---------+---------+---------+---------+ 2640
     CAATAATACCGGGAAAAGTACGACTTACATCCGTCGTGGCGGAAGTCGTGGACCACCAAC

a    V I M A L F M L N V G S T A F S T W W L -

     AGTTACTGGATCAAGCAAGGAAGCGGGAACACCACTGTGACTCGAGGGAACGAGACCTCG
2641 ---------+---------+---------+---------+---------+---------+ 2700
     TCAATGACCTAGTTCGTTCCTTCGCCCTTGTGGTGACACTGAGCTCCCTTGCTCTGGAGC

a    S Y W I K Q G S G N T T V T R G N E T S -

     GTGAGTGACAGCATGAAGGACAATCCTCATATGCAGTACTATGCCAGCATCTACGCCCTC
2701 ---------+---------+---------+---------+---------+---------+ 2760
     CACTCACTGTCGTACTTCCTGTTAGGAGTATACGTCATGATACGGTCGTAGATGCGGGAG

a    V S D S M K D N P H M Q Y Y A S I Y A L -

     TCCATGGCAGTCATGCTGATCCTGAAAGCCATTCGAGGAGTTGTCTTTGTCAAGGGCACG
2761 ---------+---------+---------+---------+---------+---------+ 2820
     AGGTACCGTCAGTACGACTAGGACTTTCGGTAAGCTCCTCAACAGAAACAGTTCCCGTGC

a    S M A V M L I L K A I R G V V F V K G T -

     CTGCGAGCTTCCTCCCGGCTGCATGACGAGCTTTTCCGAAGGATCCTTCGAAGCCCTATG
2821 ---------+---------+---------+---------+---------+---------+ 2880
     GACGCTCGAAGGAGGGCCGACGTACTGCTCGAAAAGGCTTCCTAGGAAGCTTCGGGATAC

a    L R A S S R L H D E L F R R I L R S P M -

     AAGTTTTTTGACACGACCCCCACAGGGAGGATTCTCAACAGGTTTTCCAAAGACATGGAT
2881 ---------+---------+---------+---------+---------+---------+ 2940
     TTCAAAAAACTGTGCTGGGGGTGTCCCTCCTAAGAGTTGTCCAAAAGGTTTCTGTACCTA

a    K F F D T T P T G R I L N R F S K D M D -

     GAAGTTGACGTGCGGCTGCCGTTCCAGGCCGAGATGTTCATCCAGAACGTTATCCTGGTG
```

Figure 13G

SUBSTITUTE SHEET (RULE 26)

```
2941 ---------+---------+---------+---------+---------+---------+ 3000
     CTTCAACTGCACGCCGACGGCAAGGTCCGGCTCTACAAGTAGGTCTTGCAATAGGACCAC

a    E V D V R L P F Q A E M F I Q N V I L V -

     TTCTTCTGTGTGGGAATGATCGCAGGAGTCTTCCCGTGGTTCCTTGTGGCAGTGGGGCCC
3001 ---------+---------+---------+---------+---------+---------+ 3060
     AAGAAGACACACCCTTACTAGCGTCCTCAGAAGGGCACCAAGGAACACCGTCACCCCGGG

a    F F C V G M I A G V F P W F L V A V G P -

     CTTGTCATCCTCTTTTCAGTCCTGCACATTGTCTCCAGGGTCCTGATTCGGGAGCTGAAG
3061 ---------+---------+---------+---------+---------+---------+ 3120
     GAACAGTAGGAGAAAAGTCAGGACGTGTAACAGAGGTCCCAGGACTAAGCCCTCGACTTC

a    L V I L F S V L H I V S R V L I R E L K -

     CGTCTGGACAATATCACGCAGTCACCTTTCCTCTCCCACATCACGTCCAGCATACAGGGC
3121 ---------+---------+---------+---------+---------+---------+ 3180
     GCAGACCTGTTATAGTGCGTCAGTGGAAAGGAGAGGGTGTAGTGCAGGTCGTATGTCCCG

a    R L D N I T Q S P F L S H I T S S I Q G -

     CTTGCCACCATCCACGCCTACAATAAAGGGCAGGAGTTTCTGCACAGATACCAGGAGCTG
3181 ---------+---------+---------+---------+---------+---------+ 3240
     GAACGGTGGTAGGTGCGGATGTTATTTCCCGTCCTCAAAGACGTGTCTATGGTCCTCGAC

a    L A T I H A Y N K G Q E F L H R Y Q E L -

     CTGGATGACAACCAAGCTCCTTTTTTTTTTGTTTACGTGTGCGATGCGGTGGCTGGCTGTG
3241 ---------+---------+---------+---------+---------+---------+ 3300
     GACCTACTGTTGGTTCGAGGAAAAAAAAAACAAATGCACACGCTACGCCACCGACCGACAC

a    L D D N Q A P F F L F T C A M R W L A V -

     CGGCTGGACCTCATCAGCATCGCCCTCATCACCACCACGGGGCTGATGATCGTTCTTATG
3301 ---------+---------+---------+---------+---------+---------+ 3360
     GCCGACCTGGAGTAGTCGTAGCGGGAGTAGTGGTGGTGCCCCGACTACTAGCAAGAATAC

a    R L D L I S I A L I T T T G L M I V L M -

     CACGGGCAGATTCCCCCAGCCTATGCGGGTCTCGCCATCTCTTATGCTGTCCAGTTAACG
3361 ---------+---------+---------+---------+---------+---------+ 3420
```

Figure 13H

GTGCCCGTCTAAGGGGGTCGGATACGCCCAGAGCGGTAGAGAATACGACAGGTCAATTGC

a H G Q I P P A Y A G L A I S Y A V Q L T -

GGGCTGTTCCAGTTTACGGTCAGACTGGCATCTGAGACAGAAGCTCGATTCACCTCGGTG
3421 ---------+---------+---------+---------+---------+---------+ 3480
CCCGACAAGGTCAAATGCCAGTCTGACCGTAGACTCTGTCTTCGAGCTAAGTGGAGCCAC

a G L F Q F T V R L A S E T E A R F T S V -

GAGAGGATCAATCACTACATTAAGACTCTGTCCTTGGAAGCACCTGCCAGAATTAAGAAC
3481 ---------+---------+---------+---------+---------+---------+ 3540
CTCTCCTAGTTAGTGATGTAATTCTGAGACAGGAACCTTCGTGGACGGTCTTAATTCTTG

a E R I N H Y I K T L S L E A P A R I K N -

AAGGCTCCCTCCCCTGACTGGCCCCAGGAGGGAGAGGTGACCTTTGAGAACGCAGAGATG
3541 ---------+---------+---------+---------+---------+---------+ 3600
TTCCGAGGGAGGGGACTGACCGGGGTCCTCCCTCTCCACTGGAAACTCTTGCGTCTCTAC

a K A P S P D W P Q E G E V T F E N A E M -

AGGTACCGAGAAAACCTCCCTCTTGTCCTAAAGAAAGTATCCTTCACGATCAAACCTAAA
3601 ---------+---------+---------+---------+---------+---------+ 3660
TCCATGGCTCTTTTGGAGGGAGAACAGGATTTCTTTCATAGGAAGTGCTAGTTTGGATTT

a R Y R E N L P L V L K K V S F T I K P K -

GAGAAGATTGGCATTGTGGGGCGGACAGGATCAGGGAAGTCCTCGCTGGGGATGGCCCTC
3661 ---------+---------+---------+---------+---------+---------+ 3720
CTCTTCTAACCGTAACACCCCGCCTGTCCTAGTCCCTTCAGGAGCGACCCCTACCGGGAG

a E K I G I V G R T G S G K S S L G M A L -

TTCCGTCTGGTGGAGTTATCTGGAGGCTGCATCAAGATTGATGGAGTGAGAATCAGTGAT
3721 ---------+---------+---------+---------+---------+---------+ 3780
AAGGCAGACCACCTCAATAGACCTCCGACGTAGTTCTAACTACCTCACTCTTAGTCACTA

a F R L V E L S G G C I K I D G V R I S D -

ATTGGCCTTGCCGACCTCCGAAGCAAACTCTCTATCATTCCTCAAGAGCCGGTGCTGTTC
3781 ---------+---------+---------+---------+---------+---------+ 3840
TAACCGGAACGGCTGGAGGCTTCGTTTGAGAGATAGTAAGGAGTTCTCGGCCACGACAAG

Figure 13I

```
a      I  G  L  A  D  L  R  S  K  L  S  I  I  P  Q  E  P  V  L  F  -

       AGTGGCACTGTCAGATCAAATTTGGACCCCTTCAACCAGTACACTGAAGACCAGATTTGG
  3841 ---------+---------+---------+---------+---------+---------+ 3900
       TCACCGTGACAGTCTAGTTTAAACCTGGGGAAGTTGGTCATGTGACTTCTGGTCTAAACC

a      S  G  T  V  R  S  N  L  D  P  F  N  Q  Y  T  E  D  Q  I  W  -

       GATGCCCTGGAGAGGACACACATGAAAGAATGTATTGCTCAGCTACCTCTGAAACTTGAA
  3901 ---------+---------+---------+---------+---------+---------+ 3960
       CTACGGGACCTCTCCTGTGTGTACTTTCTTACATAACGAGTCGATGGAGACTTTGAACTT

a      D  A  L  E  R  T  H  M  K  E  C  I  A  Q  L  P  L  K  L  E  -

       TCTGAAGTGATGGAGAATGGGGATAACTTCTCAGTGGGGGAACGGCAGCTCTTGTGCATA
  3961 ---------+---------+---------+---------+---------+---------+ 4020
       AGACTTCACTACCTCTTACCCCTATTGAAGAGTCACCCCCTTGCCGTCGAGAACACGTAT

a      S  E  V  M  E  N  G  D  N  F  S  V  G  E  R  Q  L  L  C  I  -

       GCTAGAGCCCTGCTCCGCCACTGTAAGATTCTGATTTTAGATGAAGCCACAGCTGCCATG
  4021 ---------+---------+---------+---------+---------+---------+ 4080
       CGATCTCGGGACGAGGCGGTGACATTCTAAGACTAAAATCTACTTCGGTGTCGACGGTAC

a      A  R  A  L  L  R  H  C  K  I  L  I  L  D  E  A  T  A  A  M  -

       GACACAGAGACAGACTTATTGATTCAAGAGACCATCCGAGAAGCATTTGCAGACTGTACC
  4081 ---------+---------+---------+---------+---------+---------+ 4140
       CTGTGTCTCTGTCTGAATAACTAAGTTCTCTGGTAGGCTCTTCGTAAACGTCTGACATGG

a      D  T  E  T  D  L  L  I  Q  E  T  I  R  E  A  F  A  D  C  T  -

       ATGCTGACCATTGCCCATCGCCTGCACACGGTTCTAGGCTCCGATAGGATTATGGTGCTG
  4141 ---------+---------+---------+---------+---------+---------+ 4200
       TACGACTGGTAACGGGTAGCGGACGTGTGCCAAGATCCGAGGCTATCCTAATACCACGAC

a      M  L  T  I  A  H  R  L  H  T  V  L  G  S  D  R  I  M  V  L  -

       GCCCAGGGACAGGTGGTGGAGTTTGACACCCCATCGGTCCTTCTGTCCAACGACAGTTCC
  4201 ---------+---------+---------+---------+---------+---------+ 4260
       CGGGTCCCTGTCCACCACCTCAAACTGTGGGGTAGCCAGGAAGACAGGTTGCTGTCAAGG
```

Figure 13J

```
a     A Q G Q V V E F D T P S V L L S N D S S -

      CGATTCTATGCCATGTTTGCTGCTGCAGAGAACAAGGTCGCTGTCAAGGGCTGA
 4261 ---------+---------+---------+---------+---------+----  4314
      GCTAAGATACGGTACAAACGACGACGTCTCTTGTTCCAGCGACAGTTCCCGACT

a     R F Y A M F A A A E N K V A V K G * -
```

Figure 13K

MOAT D cDNA AND AMINO ACID SEQUENCE ENCODED THEREBY

```
    ATGGACGCCCTGTGCGGTTCCGGGGAGCTCGGCTCCAAGTTCTGGGACTCCAACCTGTCT
  1 ---------+---------+---------+---------+---------+---------+ 60
    TACCTGCGGGACACGCCAAGGCCCCTCGAGCCGAGGTTCAAGACCCTGAGGTTGGACAGA

a   M  D  A  L  C  G  S  G  E  L  G  S  K  F  W  D  S  N  L  S  -

    GTGCACACAGAAAACCCGGACCTCACTCCCTGCTTCCAGAACTCCCTGCTGGCCTGGGTG
 61 ---------+---------+---------+---------+---------+---------+ 120
    CACGTGTGTCTTTTGGGCCTGGAGTGAGGGACGAAGGTCTTGAGGGACGACCGGACCCAC

a   V  H  T  E  N  P  D  L  T  P  C  F  Q  N  S  L  L  A  W  V  -

    CCCTGCATCTACCTGTGGGTCGCCCTGCCCTGCTACTTGCTCTACCTGCGGCACCATTGT
121 ---------+---------+---------+---------+---------+---------+ 180
    GGGACGTAGATGGACACCCAGCGGGACGGGACGATGAACGAGATGGACGCCGTGGTAACA

a   P  C  I  Y  L  W  V  A  L  P  C  Y  L  L  Y  L  R  H  H  C  -

    CGTGGCTACATCATCCTCTCCCACCTGTCCAAGCTCAAGATGGTCCTGGGTGTCCTGCTG
181 ---------+---------+---------+---------+---------+---------+ 240
    GCACCGATGTAGTAGGAGAGGGTGGACAGGTTCGAGTTCTACCAGGACCCACAGGACGAC

a   R  G  Y  I  I  L  S  H  L  S  K  L  K  M  V  L  G  V  L  L  -

    TGGTGCGTCTCCTGGGCGGACCTTTTTTACTCCTTCCATGGCCTGGTCCATGGCCGGGCC
241 ---------+---------+---------+---------+---------+---------+ 300
    ACCACGCAGAGGACCCGCCTGGAAAAAATGAGGAAGGTACCGGACCAGGTACCGGCCCGG

a   W  C  V  S  W  A  D  L  F  Y  S  F  H  G  L  V  H  G  R  A  -

    CCTGCCCCTGTTTTCTTTGTCACCCCCTTGGTGGTGGGGGTCACCATGCTGCTGGCCACC
301 ---------+---------+---------+---------+---------+---------+ 360
    GGACGGGGACAAAAGAAACAGTGGGGGAACCACCACCCCCAGTGGTACGACGACCGGTGG

a   P  A  P  V  F  F  V  T  P  L  V  V  G  V  T  M  L  L  A  T  -

    CTGCTGATACAGTATGAGCGGCTGCAGGGCGTACAGTCTTCGGGGGTCCTCATTATCTTC
```

Figure 14A

```
361 ---------+---------+---------+---------+---------+---------+ 420
    GACGACTATGTCATACTCGCCGACGTCCCGCATGTCAGAAGCCCCCAGGAGTAATAGAAG

a   L  L  I  Q  Y  E  R  L  Q  G  V  Q  S  S  G  V  L  I  I  F  -

    TGGTTCCTGTGTGTGGTCTGCGCCATCGTCCCATTCCGCTCCAAGATCCTTTTAGCCAAG
421 ---------+---------+---------+---------+---------+---------+ 480
    ACCAAGGACACACACCAGACGCGGTAGCAGGGTAAGGCGAGGTTCTAGGAAAATCGGTTC

a   W  F  L  C  V  V  C  A  I  V  P  F  R  S  K  I  L  L  A  K  -

    GCAGAGGGTGAGATCTCAGACCCCTTCCGCTTCACCACCTTCTACATCCACTTTGCCCTG
481 ---------+---------+---------+---------+---------+---------+ 540
    CGTCTCCCACTCTAGAGTCTGGGGAAGGCGAAGTGGTGGAAGATGTAGGTGAAACGGGAC

a   A  E  G  E  I  S  D  P  F  R  F  T  T  F  Y  I  H  F  A  L  -

    GTACTCTCTGCCCTCATCTTGGCCTGCTTCAGGGAGAAACCTCCATTTTTCTCCGCAAAG
541 ---------+---------+---------+---------+---------+---------+ 600
    CATGAGAGACGGGAGTAGAACCGGACGAAGTCCCTCTTTGGAGGTAAAAAGAGGCGTTTC

a   V  L  S  A  L  I  L  A  C  F  R  E  K  P  P  F  F  S  A  K  -

    AATGTCGACCCTAACCCCTACCCTGAGACCAGCGCTGGCTTTCTCTCCCGCCTGTTTTTC
601 ---------+---------+---------+---------+---------+---------+ 660
    TTACAGCTGGGATTGGGGATGGGACTCTGGTCGCGACCGAAAGAGAGGGCGGACAAAAAG

a   N  V  D  P  N  P  Y  P  E  T  S  A  G  F  L  S  R  L  F  F  -

    TGGTGGTTCACAAAGATGGCCATCTATGGCTACCGGCATCCCCTGGAGGAGAAGGACCTC
661 ---------+---------+---------+---------+---------+---------+ 720
    ACCACCAAGTGTTTCTACCGGTAGATACCGATGGCCGTAGGGGACCTCCTCTTCCTGGAG

a   W  W  F  T  K  M  A  I  Y  G  Y  R  H  P  L  E  E  K  D  L  -

    TGGTCCCTAAAGGAAGAGGACAGATCCCAGATGGTGGTGCAGCAGCTGCTGGAGGCATGG
721 ---------+---------+---------+---------+---------+---------+ 780
    ACCAGGGATTTCCTTCTCCTGTCTAGGGTCTACCACCACGTCGTCGACGACCTCCGTACC

a   W  S  L  K  E  E  D  R  S  Q  M  V  V  Q  Q  L  L  E  A  W  -

    AGGAAGCAGGAAAAGCAGACGGCACGACACAAGGCTTCAGCAGCACCTGGGAAAAATGCC
781 ---------+---------+---------+---------+---------+---------+ 840
```

Figure 14B

```
       TCCTTCGTCCTTTTCGTCTGCCGTGCTGTGTTCCGAAGTCGTCGTGGACCCTTTTTACGG

a      R  K  Q  E  K  Q  T  A  R  H  K  A  S  A  A  P  G  K  N  A  -

       TCCGGCGAGGACGAGGTGCTGCTGGGTGCCCGGCCCAGGCCCCGGAAGCCCTCCTTCCTG
   841 ---------+---------+---------+---------+---------+---------+ 900
       AGGCCGCTCCTGCTCCACGACGACCCACGGGCCGGGTCCGGGGCCTTCGGGAGGAAGGAC

a      S  G  E  D  E  V  L  L  G  A  R  P  R  P  R  K  P  S  F  L  -

       AAGGCCCTGCTGGCCACCTTCGGCTCCAGCTTCCTCATCAGTGCCTGCTTCAAGCTTATC
   901 ---------+---------+---------+---------+---------+---------+ 960
       TTCCGGGACGACCGGTGGAAGCCGAGGTCGAAGGAGTAGTCACGGACGAAGTTCGAATAG

a      K  A  L  L  A  T  F  G  S  S  F  L  I  S  A  C  F  K  L  I  -

       CAGGACCTGCTCTCCTTCATCAATCCACAGCTGCTCAGCATCCTGATCAGGTTTATCTCC
   961 ---------+---------+---------+---------+---------+---------+ 1020
       GTCCTGGACGAGAGGAAGTAGTTAGGTGTCGACGAGTCGTAGGACTAGTCCAAATAGAGG

a      Q  D  L  L  S  F  I  N  P  Q  L  L  S  I  L  I  R  F  I  S  -

       AACCCCATGGCCCCCTCCTGGTGGGGCTTCCTGGTGGCTGGGCTGATGTTCCTGTGCTCC
  1021 ---------+---------+---------+---------+---------+---------+ 1080
       TTGGGGTACCGGGGGAGGACCACCCCGAAGGACCACCGACCCGACTACAAGGACACGAGG

a      N  P  M  A  P  S  W  W  G  F  L  V  A  G  L  M  F  L  C  S  -

       ATGATGCAGTCGCTGATCTTACAACACTATTACCACTACATCTTTGTGACTGGGGTGAAG
  1081 ---------+---------+---------+---------+---------+---------+ 1140
       TACTACGTCAGCGACTAGAATGTTGTGATAATGGTGATGTAGAAACACTGACCCCACTTC

a      M  M  Q  S  L  I  L  Q  H  Y  Y  H  Y  I  F  V  T  G  V  K  -

       TTTCGTACTGGGATCATGGGTGTCATCTACAGGAAGGCTCTGGTTATCACCAACTCAGTC
  1141 ---------+---------+---------+---------+---------+---------+ 1200
       AAAGCATGACCCTAGTACCCACAGTAGATGTCCTTCCGAGACCAATAGTGGTTGAGTCAG

a      F  R  T  G  I  M  G  V  I  Y  R  K  A  L  V  I  T  N  S  V  -

       AAACGTGCGTCCACTGTGGGGGAAATTGTCAACCTCATGTCAGTGGATGCCCAGCGCTTC
  1201 ---------+---------+---------+---------+---------+---------+ 1260
       TTTGCACGCAGGTGACACCCCCTTTAACAGTTGGAGTACAGTCACCTACGGGTCGCGAAG
```

Figure 14C

```
a      K  R  A  S  T  V  G  E  I  V  N  L  M  S  V  D  A  Q  R  F  -

       ATGGACCTTGCCCCCTTCCTCAATCTGCTGTGGTCAGCACCCCTGCAGATCATCCTGGCG
  1261 ---------+---------+---------+---------+---------+---------+  1320
       TACCTGGAACGGGGGAAGGAGTTAGACGACACCAGTCGTGGGGACGTCTAGTAGGACCGC

a      M  D  L  A  P  F  L  N  L  L  W  S  A  P  L  Q  I  I  L  A  -

       ATCTACTTCCTCTGGCAGAACCTAGGTCCCTCTGTCCTGGCTGGAGTCGCTTTCATGGTC
  1321 ---------+---------+---------+---------+---------+---------+  1380
       TAGATGAAGGAGACCGTCTTGGATCCAGGGAGACAGGACCGACCTCAGCGAAAGTACCAG

a      I  Y  F  L  W  Q  N  L  G  P  S  V  L  A  G  V  A  F  M  V  -

       TTGCTGATTCCACTCAACGGAGCTGTGGCCGTGAAGATGCGCGCCTTCCAGGTAAAGCAA
  1381 ---------+---------+---------+---------+---------+---------+  1440
       AACGACTAAGGTGAGTTGCCTCGACACCGGCACTTCTACGCGCGGAAGGTCCATTTCGTT

a      L  L  I  P  L  N  G  A  V  A  V  K  M  R  A  F  Q  V  K  Q  -

       ATGAAATTGAAGGACTCGCGCATCAAGCTGATGAGTGAGATCCTGAACGGCATCAAGGTG
  1441 ---------+---------+---------+---------+---------+---------+  1500
       TACTTTAACTTCCTGAGCGCGTAGTTCGACTACTCACTCTAGGACTTGCCGTAGTTCCAC

a      M  K  L  K  D  S  R  I  K  L  M  S  E  I  L  N  G  I  K  V  -

       CTGAAGCTGTACGCCTGGGAGCCCAGCTTCCTGAAGCAGGTGGAGGGCATCCGGCAGGGT
  1501 ---------+---------+---------+---------+---------+---------+  1560
       GACTTCGACATGCGGACCCTCGGGTCGAAGGACTTCGTCCACCTCCCGTAGGCCGTCCCA

a      L  K  L  Y  A  W  E  P  S  F  L  K  Q  V  E  G  I  R  Q  G  -

       GAGCTCCAGCTGCTGCGCACGGCGGCCTACCTCCACACCACAACCACCTTCACCTGGATG
  1561 ---------+---------+---------+---------+---------+---------+  1620
       CTCGAGGTCGACGACGCGTGCCGCCGGATGGAGGTGTGGTGTTGGTGGAAGTGGACCTAC

a      E  L  Q  L  L  R  T  A  A  Y  L  H  T  T  T  T  F  T  W  M  -

       TGCAGCCCCTTCCTGGTGACCCTGATCACCCTCTGGGTGTACGTGTACGTGGACCCAAAC
  1621 ---------+---------+---------+---------+---------+---------+  1680
       ACGTCGGGGAAGGACCACTGGGACTAGTGGGAGACCCACATGCACATGCACCTGGGTTTG
```

Figure 14D

SUBSTITUTE SHEET (RULE 26)

```
a     C S P F L V T L I T L W V Y Y V Y V D P N -

      AATGTGCTGGACGCCGAGAAGGCCTTTGTGTCTGTGTCCTTGTTTAATATCTTAAGACTT
 1681 ---------+---------+---------+---------+---------+---------+  1740
      TTACACGACCTGCGGCTCTTCCGGAAACACAGACACAGGAACAAATTATAGAATTCTGAA

a     N V L D A E K A F V S V S L F N I L R L -

      CCCCTCAACATGCTGCCCCAGTTAATCAGCAACCTGACTCAGGCCAGTGTGTCTCTGAAA
 1741 ---------+---------+---------+---------+---------+---------+  1800
      GGGGAGTTGTACGACGGGGTCAATTAGTCGTTGGACTGAGTCCGGTCACACAGAGACTTT

a     P L N M L P Q L I S N L T Q A S V S L K -

      CGGATCCAGCAATTCCTGAGCCAAGAGGAACTTGACCCCCAGAGTGTGGAAAGAAAGACC
 1801 ---------+---------+---------+---------+---------+---------+  1860
      GCCTAGGTCGTTAAGGACTCGGTTCTCCTTGAACTGGGGGTCTCACACCTTTCTTTCTGG

a     R I Q Q F L S Q E E L D P Q S V E R K T -

      ATCTCCCCAGGCTATGCCATCACCATACACAGTGGCACCTTCACCTGGGCCCAGGACCTG
 1861 ---------+---------+---------+---------+---------+---------+  1920
      TAGAGGGGTCCGATACGGTAGTGGTATGTGTCACCGTGGAAGTGGACCCGGGTCCTGGAC

a     I S P G Y A I T I H S G T F T W A Q D L -

      CCCCCCACTCTGCACAGCCTAGACATCCAGGTCCCGAAAGGGGCACTGGTGGCCGTGGTG
 1921 ---------+---------+---------+---------+---------+---------+  1980
      GGGGGGTGAGACGTGTCGGATCTGTAGGTCCAGGGCTTTCCCCGTGACCACCGGCACCAC

a     P P T L H S L D I Q V P K G A L V A V V -

      GGGCCTGTGGGCTGTGGGAAGTCCTCCCTGGTGTCTGCCCTGCTGGGAGAGATGGAGAAG
 1981 ---------+---------+---------+---------+---------+---------+  2040
      CCCGGACACCCGACACCCTTCAGGAGGGACCACAGACGGGACGACCCTCTCTACCTCTTC

a     G P V G C G K S S L V S A L L G E M E K -

      CTAGAAGGCAAAGTGCACATGAAGGCATGGATCCAGAACTGCACTCTTCAGGAAAACGTG
 2041 ---------+---------+---------+---------+---------+---------+  2100
      GATCTTCCGTTTCACGTGTACTTCCGTACCTAGGTCTTGACGTGAGAAGTCCTTTTGCAC

a     L E G K V H M K A W I Q N C T L Q E N V -
```

Figure 14E

```
      CTTTTCGGCAAAGCCCTGAACCCCAAGCGCTACCAGCAGACTCTGGAGGCCTGTGCCTTG
2101 ---------+---------+---------+---------+---------+---------+ 2160
      GAAAAGCCGTTTCGGGACTTGGGGTTCGCGATGGTCGTCTGAGACCTCCGGACACGGAAC

a     L  F  G  K  A  L  N  P  K  R  Y  Q  Q  T  L  E  A  C  A  L  -

      CTAGCTGACCTGGAGATGCTGCCTGGTGGGGATCAGACAGAGATTGGAGAGAAGGGCATT
2161 ---------+---------+---------+---------+---------+---------+ 2220
      GATCGACTGGACCTCTACGACGGACCACCCCTAGTCTGTCTCTAACCTCTCTTCCCGTAA

a     L  A  D  L  E  M  L  P  G  G  D  Q  T  E  I  G  E  K  G  I  -

      AACCTGTCTGGGGGCCAGCGGCAGCGGGTCAGTCTGGCTCGAGCTGTTTACAGTGATGCC
2221 ---------+---------+---------+---------+---------+---------+ 2280
      TTGGACAGACCCCCGGTCGCCGTCGCCCAGTCAGACCGAGCTCGACAAATGTCACTACGG

a     N  L  S  G  G  Q  R  Q  R  V  S  L  A  R  A  V  Y  S  D  A  -

      GATATTTTCTTGCTGGATGACCCACTGTCCGCGGTGGACTCTCATGTGGCCAAGCACATC
2281 ---------+---------+---------+---------+---------+---------+ 2340
      CTATAAAAGAACGACCTACTGGGTGACAGGCGCCACCTGAGAGTACACCGGTTCGTGTAG

a     D  I  F  L  L  D  D  P  L  S  A  V  D  S  H  V  A  K  H  I  -

      TTTGACCACGTCATCGGGCCAGAAGGCGTGCTGGCAGGCAAGACGCGAGTGCTGGTGACG
2341 ---------+---------+---------+---------+---------+---------+ 2400
      AAACTGGTGCAGTAGCCCGGTCTTCCGCACGACCGTCCGTTCTGCGCTCACGACCACTGC

a     F  D  H  V  I  G  P  E  G  V  L  A  G  K  T  R  V  L  V  T  -

      CACGGCATTAGCTTCCTGCCCCAGACAGACTTCATCATTGTGCTAGCTGATGGACAGGTG
2401 ---------+---------+---------+---------+---------+---------+ 2460
      GTGCCGTAATCGAAGGACGGGGTCTGTCTGAAGTAGTAACACGATCGACTACCTGTCCAC

a     H  G  I  S  F  L  P  Q  T  D  F  I  I  V  L  A  D  G  Q  V  -

      TCTGAGATGGGCCCGTACCCAGCCCTGCTGCAGCGCAACGGCTCCTTTGCCAACTTTCTC
2461 ---------+---------+---------+---------+---------+---------+ 2520
      AGACTCTACCCGGGCATGGGTCGGGACGACGTCGCGTTGCCGAGGAAACGGTTGAAAGAG

a     S  E  M  G  P  Y  P  A  L  L  Q  R  N  G  S  F  A  N  F  L  -
```

Figure 14F

```
     TGCAACTATGCCCCCGATGAGGACCAAGGGCACCTGGAGGACAGCTGGACCGCGTTGGAA
2521 ---------+---------+---------+---------+---------+---------+ 2580
     ACGTTGATACGGGGGCTACTCCTGGTTCCCGTGGACCTCCTGTCGACCTGGCGCAACCTT

a    C N Y A P D E D Q G H L E D S W T A L E -

     GGTGCAGAGGATAAGGAGGCACTGCTGATTGAAGACACACTCAGCAACCACACGGATCTG
2581 ---------+---------+---------+---------+---------+---------+ 2640
     CCACGTCTCCTATTCCTCCGTGACGACTAACTTCTGTGTGAGTCGTTGGTGTGCCTAGAC

a    G A E D K E A L L I E D T L S N H T D L -

     ACAGACAATGATCCAGTCACCTATGTGGTCCAGAAGCAGTTTATGAGACAGCTGAGTGCC
2641 ---------+---------+---------+---------+---------+---------+ 2700
     TGTCTGTTACTAGGTCAGTGGATACACCAGGTCTTCGTCAAATACTCTGTCGACTCACGG

a    T D N D P V T Y V V Q K Q F M R Q L S A -

     CTGTCCTCAGATGGGGAGGGACAGGGTCGGCCTGTACCCCGGAGGCACCTGGGTCCATCA
2701 ---------+---------+---------+---------+---------+---------+ 2760
     GACAGGAGTCTACCCCTCCCTGTCCCAGCCGGACATGGGGCCTCCGTGGACCCAGGTAGT

a    L S S D G E G Q G R P V P R R H L G P S -

     GAGAAGGTGCAGGTGACAGAGGCGAAGGCAGATGGGGCACTGACCCAGGAGGAGAAAGCA
2761 ---------+---------+---------+---------+---------+---------+ 2820
     CTCTTCCACGTCCACTGTCTCCGCTTCCGTCTACCCCGTGACTGGGTCCTCCTCTTTCGT

a    E K V Q V T E A K A D G A L T Q E E K A -

     GCCATTGGCACTGTGGAGCTCAGTGTGTTCTGGGATTATGCCAAGGCCGTGGGGCTCTGT
2821 ---------+---------+---------+---------+---------+---------+ 2880
     CGGTAACCGTGACACCTCGAGTCACACAAGACCCTAATACGGTTCCGGCACCCCGAGACA

a    A I G T V E L S V F W D Y A K A V G L C -

     ACCACGCTGGCCATCTGTCTCCTGTATGTGGGTCAAAGTGCGGCTGCCATTGGAGCCAAT
2881 ---------+---------+---------+---------+---------+---------+ 2940
     TGGTGCGACCGGTAGACAGAGGACATACACCCAGTTTCACGCCGACGGTAACCTCGGTTA

a    T T L A I C L L Y V G Q S A A A I G A N

     GTGTGGCTCAGTGCCTGGACAAATGATGCCATGGCAGACAGTAGACAGAACAACACTTCC
```

Figure 14G

SUBSTITUTE SHEET (RULE 26)

```
2941 ---------+---------+---------+---------+---------+---------+ 3000
     CACACCGAGTCACGGACCTGTTTACTACGGTACCGTCTGTCATCTGTCTTGTTGTGAAGG

a    V  W  L  S  A  W  T  N  D  A  M  A  D  S  R  Q  N  N  T  S  -

     CTGAGGCTGGGCGTCTATGCTGCTTTAGGAATTCTGCAAGGGTTCTTGGTGATGCTGGCA
3001 ---------+---------+---------+---------+---------+---------+ 3060
     GACTCCGACCCGCAGATACGACGAAATCCTTAAGACGTTCCCAAGAACCACTACGACCGT

a    L  R  L  G  V  Y  A  A  L  G  I  L  Q  G  F  L  V  M  L  A  -

     GCCATGGCCATGGCAGCGGGTGGCATCCAGGCTGCCCGTGTGTTGCACCAGGCACTGCTG
3061 ---------+---------+---------+---------+---------+---------+ 3120
     CGGTACCGGTACCGTCGCCCACCGTAGGTCCGACGGGCACACAACGTGGTCCGTGACGAC

a    A  M  A  M  A  A  G  G  I  Q  A  A  R  V  L  H  Q  A  L  L  -

     CACAACAAGATACGCTCGCCACAGTCCTTCTTTGACACCACACCATCAGGCCGCATCCTG
3121 ---------+---------+---------+---------+---------+---------+ 3180
     GTGTTGTTCTATGCGAGCGGTGTCAGGAAGAAACTGTGGTGTGGTAGTCCGGCGTAGGAC

a    H  N  K  I  R  S  P  Q  S  F  F  D  T  T  P  S  G  R  I  L  -

     AACTGCTTCTCCAAGGACATCTATGTCGTTGATGAGGTTCTGGCCCCTGTCATCCTCATG
3181 ---------+---------+---------+---------+---------+---------+ 3240
     TTGACGAAGAGGTTCCTGTAGATACAGCAACTACTCCAAGACCGGGGACAGTAGGAGTAC

a    N  C  F  S  K  D  I  Y  V  V  D  E  V  L  A  P  V  I  L  M  -

     CTGCTCAATTCCTTCTTCAACGCCATCTCCACTCTTGTGGTCATCATGGCCAGCACGCCG
3241 ---------+---------+---------+---------+---------+---------+ 3300
     GACGAGTTAAGGAAGAAGTTGCGGTAGAGGTGAGAACACCAGTAGTACCGGTCGTGCGGC

a    L  L  N  S  F  F  N  A  I  S  T  L  V  V  I  M  A  S  T  P  -

     CTCTTCACTGTGGTCATCCTGCCCCTGGCTGTGCTCTACACCTTAGTGCAGCGCTTCTAT
3301 ---------+---------+---------+---------+---------+---------+ 3360
     GAGAAGTGACACCAGTAGGACGGGGACCGACACGAGATGTGGAATCACGTCGCGAAGATA

a    L  F  T  V  V  I  L  P  L  A  V  L  Y  T  L  V  Q  R  F  Y  -

     GCAGCCACATCACGGCAACTGAAGCGGCTGGAATCAGTCAGCCGCTCACCTATCTACTCC
3361 ---------+---------+---------+---------+---------+---------+ 3420
```

Figure 14H

```
     CGTCGGTGTAGTGCCGTTGACTTCGCCGACCTTAGTCAGTCGGCGAGTGGATAGATGAGG

a    A  A  T  S  R  Q  L  K  R  L  E  S  V  S  R  S  P  I  Y  S  -

     CACTTTTCGGAGACAGTGACTGGTGCCAGTGTCATCCGGGCCTACAACCGCAGCCGGGAT
3421 ---------+---------+---------+---------+---------+---------+ 3480
     GTGAAAAGCCTCTGTCACTGACCACGGTCACAGTAGGCCCGGATGTTGGCGTCGGCCCTA

a    H  F  S  E  T  V  T  G  A  S  V  I  R  A  Y  N  R  S  R  D  -

     TTTGAGATCATCAGTGATACTAAGGTGGATGCCAACCAGAGAAGCTGCTACCCCTACATC
3481 ---------+---------+---------+---------+---------+---------+ 3540
     AAACTCTAGTAGTCACTATGATTCCACCTACGGTTGGTCTCTTCGACGATGGGGATGTAG

a    F  E  I  I  S  D  T  K  V  D  A  N  Q  R  S  C  Y  P  Y  I  -

     ATCTCCAACCGGTGGCTGAGCATCGGAGTGGAGTTCGTGGGGAACTGCGTGGTGCTCTTT
3541 ---------+---------+---------+---------+---------+---------+ 3600
     TAGAGGTTGGCCACCGACTCGTAGCCTCACCTCAAGCACCCCTTGACGCACCACGAGAAA

a    I  S  N  R  W  L  S  I  G  V  E  F  V  G  N  C  V  V  L  F  -

     GCTGCACTATTTGCCGTCATCGGGAGGAGCAGCCTGAACCCGGGGCTGGTGGGCCTTTCT
3601 ---------+---------+---------+---------+---------+---------+ 3660
     CGACGTGATAAACGGCAGTAGCCCTCCTCGTCGGACTTGGGCCCCGACCACCCGGAAAGA

a    A  A  L  F  A  V  I  G  R  S  S  L  N  P  G  L  V  G  L  S  -

     GTGTCCTACTCCTTGCAGGTGACATTTGCTCTGAACTGGATGATACGAATGATGTCAGAT
3661 ---------+---------+---------+---------+---------+---------+ 3720
     CACAGGATGAGGAACGTCCACTGTAAACGAGACTTGACCTACTATGCTTACTACAGTCTA

a    V  S  Y  S  L  Q  V  T  F  A  L  N  W  M  I  R  M  M  S  D  -

     TTGGAATCTAACATCGTGGCTGTGGAGAGGGTCAAGGAGTACTCCAAGACAGAGACAGAG
3721 ---------+---------+---------+---------+---------+---------+ 3780
     AACCTTAGATTGTAGCACCGACACCTCTCCCAGTTCCTCATGAGGTTCTGTCTCTGTCTC

a    L  E  S  N  I  V  A  V  E  R  V  K  E  Y  S  K  T  E  T  E  -

     GCGCCCTGGGTGGTGGAAGGCAGCCGCCCTCCCGAAGGTTGGCCCCCACGTGGGGAGGTG
3781 ---------+---------+---------+---------+---------+---------+ 3840
     CGCGGGACCCACCACCTTCCGTCGGCGGGAGGGCTTCCAACCGGGGGTGCACCCCTCCAC
```

Figure 14I

```
a     A P W V V E G S R P P E G W P P R G E V -

      GAGTTCCGGAATTATTCTGTGCGCTACCGGCCGGGCCTAGACCTGGTGCTGAGAGACCTG
 3841 ---------+---------+---------+---------+---------+---------+ 3900
      CTCAAGGCCTTAATAAGACACGCGATGGCCGGCCCGGATCTGGACCACGACTCTCTGGAC

a     E F R N Y S V R Y R P G L D L V L R D L -

      AGTCTGCATGTGCACGGTGGCGAGAAGGTGGGGATCGTGGGCCGCACTGGGGCTGGCAAG
 3901 ---------+---------+---------+---------+---------+---------+ 3960
      TCAGACGTACACGTGCCACCGCTCTTCCACCCCTAGCACCCGGCGTGACCCCGACCGTTC

a     S L H V H G G E K V G I V G R T G A G K -

      TCTTCCATGACCCTTTGCCTGTTCCGCATCCTGGAGGCGGCAAAGGGTGAAATCCGCATT
 3961 ---------+---------+---------+---------+---------+---------+ 4020
      AGAAGGTACTGGGAAACGGACAAGGCGTAGGACCTCCGCCGTTTCCCACTTTAGGCGTAA

a     S S M T L C L F R I L E A A K G E I R I -

      GATGGCCTCAATGTGGCAGACATCGGCCTCCATGACCTGCGCTCTCAGCTGACCATCATC
 4021 ---------+---------+---------+---------+---------+---------+ 4080
      CTACCGGAGTTACACCGTCTGTAGCCGGAGGTACTGGACGCGAGAGTCGACTGGTAGTAG

a     D G L N V A D I G L H D L R S Q L T I I -

      CCGCAGGACCCCATCCTGTTCTCGGGGACCCTGCGCATGAACCTGGACCCCTTCGGCAGC
 4081 ---------+---------+---------+---------+---------+---------+ 4140
      GGCGTCCTGGGGTAGGACAAGAGCCCCTGGGACGCGTACTTGGACCTGGGGAAGCCGTCG

a     P Q D P I L F S G T L R M N L D P F G S -

      TACTCAGAGGAGGACATTTGGTGGGCTTTGGAGCTGTCCCACCTGCACACGTTTGTGAGC
 4141 ---------+---------+---------+---------+---------+---------+ 4200
      ATGAGTCTCCTCCTGTAAACCACCCGAAACCTCGACAGGGTGGACGTGTGCAAACACTCG

a     Y S E E D I W W A L E L S H L H T F V S -

      TCCCAGCCGGCAGGCCTGGACTTCCAGTGCTCAGAGGGCGGGGAGAATCTCAGCGTGGGC
 4201 ---------+---------+---------+---------+---------+---------+ 4260
      AGGGTCGGCCGTCCGGACCTGAAGGTCACGAGTCTCCCGCCCCTCTTAGAGTCGCACCCG
```

Figure 14J

```
a     S Q P A G L D F Q C S E G G E N L S V G -

      CAGAGGCAGCTCGTGTGCCTGGCCCGAGCCCTGCTCCGCAAGAGCCGCATCCTGGTTTTA
 4261 ---------+---------+---------+---------+---------+---------+ 4320
      GTCTCCGTCGAGCACACGGACCGGGCTCGGGACGAGGCGTTCTCGGCGTAGGACCAAAAT

a     Q R Q L V C L A R A L L R K S R I L V L -

      GACGAGGCCACAGCTGCCATCGACCTGGAGACTGACAACCTCATCCAGGCTACCATCCGC
 4321 ---------+---------+---------+---------+---------+---------+ 4380
      CTGCTCCGGTGTCGACGGTAGCTGGACCTCTGACTGTTGGAGTAGGTCCGATGGTAGGCG

a     D E A T A A I D L E T D N L I Q A T I R -

      ACCCAGTTTGATACCTGCACTGTCCTGACCATCGCACACCGGCTTAACACTATCATGGAC
 4381 ---------+---------+---------+---------+---------+---------+ 4440
      TGGGTCAAACTATGGACGTGACAGGACTGGTAGCGTGTGGCCGAATTGTGATAGTACCTG

a     T Q F D T C T V L T I A H R L N T I M D -

      TACACCAGGGTCCTGGTCCTGGACAAAGGAGTAGTAGCTGAATTTGATTCTCCAGCCAAC
 4441 ---------+---------+---------+---------+---------+---------+ 4500
      ATGTGGTCCCAGGACCAGGACCTGTTTCCTCATCATCGACTTAAACTAAGAGGTCGGTTG

a     Y T R V L V L D K G V V A E F D S P A N -

      CTCATTGCAGCTAGAGGCATCTTCTACGGGATGGCCAGAGATGCTGGACTTGCCTAA
 4501 ---------+---------+---------+---------+---------+------ 4557
      GAGTAACGTCGATCTCCGTAGAAGATGCCCTACCGGTCTCTACGACCTGAACGGATT

a     L I A A R G I F Y G M A R D A G L A * -
```

Figure 14K

MOAT E cDNA AND AMINO ACID SEQUENCE ENCODED THEREBY

```
    ATGGCCGCGCCTGCTGAGCCCTGCGCGGGGCAGGGGGTCTGGAACCAGACAGAGCCTGAA
  1 ---------+---------+---------+---------+---------+---------+ 60
    TACCGGCGCGGACGACTCGGGACGCGCCCCGTCCCCCAGACCTTGGTCTGTCTCGGACTT

a   M A A P A E P C A G Q G V W N Q T E P E -

    CCTGCCGCCACCAGCCTGCTGAGCCTGTGCTTCCTGAGAACAGCAGGGGTCTGGGTACCC
 61 ---------+---------+---------+---------+---------+---------+ 120
    GGACGGCGGTGGTCGGACGACTCGGACACGAAGGACTCTTGTCGTCCCCAGACCCATGGG

a   P A A T S L L S L C F L R T A G V W V P -

    CCCATGTACCTCTGGGTCCTTGGTCCCATCTACCTCCTCTTCATCCACCACCATGGCCGG
121 ---------+---------+---------+---------+---------+---------+ 180
    GGGTACATGGAGACCCAGGAACCAGGGTAGATGGAGGAGAAGTAGGTGGTGGTACCGGCC

a   P M Y L W V L G P I Y L L F I H H H G R -

    GGCTACCTCCGGATGTCCCCACTCTTCAAAGCCAAGATGGTGCTTGGATTCGCCCTCATA
181 ---------+---------+---------+---------+---------+---------+ 240
    CCGATGGAGGCCTACAGGGGTGAGAAGTTTCGGTTCTACCACGAACCTAAGCGGGAGTAT

a   G Y L R M S P L F K A K M V L G F A L I -

    GTCCTGTGTACCTCCAGCGTGGCTGTCGCTCTTTGGAAAATCCAACAGGGAACGCCTGAG
241 ---------+---------+---------+---------+---------+---------+ 300
    CAGGACACATGGAGGTCGCACCGACAGCGAGAAACCTTTTAGGTTGTCCCTTGCGGACTC

a   V L C T S S V A V A L W K I Q Q G T P E -

    GCCCCAGAATTCCTCATTCATCCTACTGTGTGGCTCACCACGATGAGCTTCGCAGTGTTC
301 ---------+---------+---------+---------+---------+---------+ 360
    CGGGGTCTTAAGGAGTAAGTAGGATGACACACCGAGTGGTGCTACTCGAAGCGTCACAAG

a   A P E F L I H P T V W L T T M S F A V F -

    CTGATTCACACCGAGAGGAAAAAGGGAGTCCAGTCATCTGGAGTGCTGTTTGGTTACTGG
361 ---------+---------+---------+---------+---------+---------+ 420
    GACTAAGTGTGGCTCTCCTTTTTCCCTCAGGTCAGTAGACCTCACGACAAACCAATGACC
```

Figure 15A

```
a     L I H T E R K K G V Q S S G V L F G Y W -

      CTTCTCTGCTTTGTCTTGCCAGCTACCAACGCTGCCCAGCAGGCCTCCGGAGCGGGCTTC
  421 ---------+---------+---------+---------+---------+---------+      480
      GAAGAGACGAAACAGAACGGTCGATGGTTGCGACGGGTCGTCCGGAGGCCTCGCCCGAAG

a     L L C F V L P A T N A A Q Q A S G A G F -

      CAGAGCGACCCTGTCCGCCACCTGTCCACCTACCTATGCCTGTCTCTGGTGGTGGCACAG
  481 ---------+---------+---------+---------+---------+---------+      540
      GTCTCGCTGGGACAGGCGGTGGACAGGTGGATGGATACGGACAGAGACCACCACCGTGTC

a     Q S D P V R H L S T Y L C L S L V V A Q -

      TTTGTGCTGTCCTGCCTGGCGGATCAACCCCCCTTCTTCCCTGAAGACCCCCAGCAGTCT
  541 ---------+---------+---------+---------+---------+---------+      600
      AAACACGACAGGACGGACCGCCTAGTTGGGGGGAAGAAGGGACTTCTGGGGGTCGTCAGA

a     F V L S C L A D Q P P F F P E D P Q Q S -

      AACCCCTGTCCAGAGACTGGGGCAGCCTTCCCCTCCAAAGCCACGTTCTGGTGGGTTTCT
  601 ---------+---------+---------+---------+---------+---------+      660
      TTGGGGACAGGTCTCTGACCCCGTCGGAAGGGGAGGTTTCGGTGCAAGACCACCCAAAGA

a     N P C P E T G A A F P S K A T F W W V S -

      GGCCTGGTCTGGAGGGGATACAGGAGGCCACTGAGACCAAAAGACCTCTGGTCGCTTGGG
  661 ---------+---------+---------+---------+---------+---------+      720
      CCGGACCAGACCTCCCCTATGTCCTCCGGTGACTCTGGTTTTCTGGAGACCAGCGAACCC

a     G L V W R G Y R R P L R P K D L W S L G -

      AGAGAAAACTCCTCAGAAGAACTTGTTTCCCGGCTTGAAAAGGAGTGGATGAGGAACCGC
  721 ---------+---------+---------+---------+---------+---------+      780
      TCTCTTTTGAGGAGTCTTCTTGAACAAAGGGCCGAACTTTTCCTCACCTACTCCTTGGCG

a     R E N S S E E L V S R L E K E W M R N R -

      AGTGCAGCCCGGAGGCACAACAAGGCAATAGCATTTAAAAGGAAAGGCGGCAGTGGCATG
  781 ---------+---------+---------+---------+---------+---------+      840
      TCACGTCGGGCCTCCGTGTTGTTCCGTTATCGTAAATTTTCCTTTCCGCCGTCACCGTAC
```

Figure 15B

```
a     S A A R R H N K A I A F K R K G G S G M -

      AAGGCTCCAGAGACCGAGCCCTTCCTACGGCAAGAAGGGAGCCAGTGGCGCCCACTGCTG
 841 ---------+---------+---------+---------+---------+---------+ 900
      TTCCGAGGTCTCTGGCTCGGGAAGGATGCCGTTCTTCCCTCGGTCACCGCGGGTGACGAC

a     K A P E T E P F L R Q E G S Q W R P L L -

      AAGGCCATCTGGCAGGTGTTCCATTCTACCTTCCTCCTGGGGACCCTCAGCCTCATCATC
 901 ---------+---------+---------+---------+---------+---------+ 960
      TTCCGGTAGACCGTCCACAAGGTAAGATGGAAGGAGGACCCCTGGGAGTCGGAGTAGTAG

a     K A I W Q V F H S T F L L G T L S L I I -

      AGTGATGTCTTCAGGTTCACTGTCCCCAAGCTGCTCAGCCTTTTCCTGGAGTTTATTGGT
 961 ---------+---------+---------+---------+---------+---------+ 1020
      TCACTACAGAAGTCCAAGTGACAGGGGTTCGACGAGTCGGAAAAGGACCTCAAATAACCA

a     S D V F R F T V P K L L S L F L E F I G -

      GATCCCAAGCCTCCAGCCTGGAAGGGCTACCTCCTCGCCGTGCTGATGTTCCTCTCAGCC
1021 ---------+---------+---------+---------+---------+---------+ 1080
      CTAGGGTTCGGAGGTCGGACCTTCCCGATGGAGGAGCGGCACGACTACAAGGAGAGTCGG

a     D P K P P A W K G Y L L A V L M F L S A -

      TGCCTGCAAACGCTGTTTGAGCAGCAGAACATGTACAGGCTCAAGGTGCCGCAGATGAGG
1081 ---------+---------+---------+---------+---------+---------+ 1140
      ACGGACGTTTGCGACAAACTCGTCGTCTTGTACATGTCCGAGTTCCACGGCGTCTACTCC

a     C L Q T L F E Q Q N M Y R L K V P Q M R -

      TTGCGGTCGGCCATCACTGGCCTGGTGTACAGAAAGGTCCTGGCTCTGTCCAGCGGCTCC
1141 ---------+---------+---------+---------+---------+---------+ 1200
      AACGCCAGCCGGTAGTGACCGGACCACATGTCTTTCCAGGACCGAGACAGGTCGCCGAGG

a     L R S A I T G L V Y R K V L A L S S G S -

      AGAAAGGCCAGTGCGGTGGGTGATGTGGTCAATCTGGTGTCCGTGGACGTGCAGCGGCTG
1201 ---------+---------+---------+---------+---------+---------+ 1260
      TCTTTCCGGTCACGCCACCCACTACACCAGTTAGACCACAGGCACCTGCACGTCGCCGAC

a     R K A S A V G D V V N L V S V D V Q R L -
```

Figure 15C

```
      ACCGAGAGCGTCCTCTACCTCAACGGGCTGTGGCTGCCTCTCGTCTGGATCGTGGTCTGC
 1261 ---------+---------+---------+---------+---------+---------+ 1320
      TGGCTCTCGCAGGAGATGGAGTTGCCCGACACCGACGGAGAGCAGACCTAGCACCAGACG

a     T  E  S  V  L  Y  L  N  G  L  W  L  P  L  V  W  I  V  V  C  -

      TTCGTCTATCTCTGGCAGCTCCTGGGGCCCTCCGCCCTCACTGCCATCGCTGTCTTCCTG
 1321 ---------+---------+---------+---------+---------+---------+ 1380
      AAGCAGATAGAGACCGTCGAGGACCCCGGGAGGCGGGAGTGACGGTAGCGACAGAAGGAC

a     F  V  Y  L  W  Q  L  L  G  P  S  A  L  T  A  I  A  V  F  L  -

      AGCCTCCTCCCTCTGAATTTCTTCATCTCCAAGAAAAGGAACCACCATCAGGAGGAGCAA
 1381 ---------+---------+---------+---------+---------+---------+ 1440
      TCGGAGGAGGGAGACTTAAAGAAGTAGAGGTTCTTTTCCTTGGTGGTAGTCCTCCTCGTT

a     S  L  L  P  L  N  F  F  I  S  K  K  R  N  H  H  Q  E  E  Q  -

      ATGAGGCAGAAGGACTCACGGGCACGGCTCACCAGCTCTATCCTCAGGAACTCGAAGACC
 1441 ---------+---------+---------+---------+---------+---------+ 1500
      TACTCCGTCTTCCTGAGTGCCCGTGCCGAGTGGTCGAGATAGGAGTCCTTGAGCTTCTGG

a     M  R  Q  K  D  S  R  A  R  L  T  S  S  I  L  R  N  S  K  T  -

      ATCAAGTTCCATGGCTGGGAGGGAGCCTTTCTGGACAGAGTCCTGGGCATCCGAGGCCAG
 1501 ---------+---------+---------+---------+---------+---------+ 1560
      TAGTTCAAGGTACCGACCCTCCCTCGGAAAGACCTGTCTCAGGACCCGTAGGCTCCGGTC

a     I  K  F  H  G  W  E  G  A  F  L  D  R  V  L  G  I  R  G  Q  -

      GAGCTGGGCGCCTTGCGGACCTCCGGCCTCCTCTTCTCTGTGTCGCTGGTGTCCTTCCAA
 1561 ---------+---------+---------+---------+---------+---------+ 1620
      CTCGACCCGCGGAACGCCTGGAGGCCGGAGGAGAAGAGACACAGCGACCACAGGAAGGTT

a     E  L  G  A  L  R  T  S  G  L  L  F  S  V  S  L  V  S  F  Q  -

      GTGTCTACATTTCTGGTCGCACTGGTGGTGTTTGCTGTCCACACTCTGGTGGCCGAGAAT
 1621 ---------+---------+---------+---------+---------+---------+ 1680
      CACAGATGTAAAGACCAGCGTGACCACCACAAACGACAGGTGTGAGACCACCGGCTCTTA

a     V  S  T  F  L  V  A  L  V  V  F  A  V  H  T  L  V  A  E  N  -
```

Figure 15D

```
     GCTATGAATGCAGAGAAAGCCTTTGTGACTCTCACAGTTCTCAACATCCTCAACAAGGCC
1681 ---------+---------+---------+---------+---------+---------+ 1740
     CGATACTTACGTCTCTTTCGGAAACACTGAGAGTGTCAAGAGTTGTAGGAGTTGTTCCGG

a    A  M  N  A  E  K  A  F  V  T  L  T  V  L  N  I  L  N  K  A  -

     CAGGCTTTCCTGCCCTTCTCCATCCACTCCCTCGTCCAGGCCCGGGTGTCCTTTGACCGT
1741 ---------+---------+---------+---------+---------+---------+ 1800
     GTCCGAAAGGACGGGAAGAGGTAGGTGAGGGAGCAGGTCCGGGCCCACAGGAAACTGGCA

a    Q  A  F  L  P  F  S  I  H  S  L  V  Q  A  R  V  S  F  D  R  -

     CTGGTCACCTTCCTCTGCCTGGAAGAAGTTGACCCTGGTGTCGTAGACTCAAGTTCCTCT
1801 ---------+---------+---------+---------+---------+---------+ 1860
     GACCAGTGGAAGGAGACGGACCTTCTTCAACTGGGACCACAGCATCTGAGTTCAAGGAGA

a    L  V  T  F  L  C  L  E  E  V  D  P  G  V  V  D  S  S  S  S  -

     GGAAGCGCTGCCGGGAAGGATTGCATCACCATACACAGTGCCACCTTCGCCTGGTCCCAG
1861 ---------+---------+---------+---------+---------+---------+ 1920
     CCTTCGCGACGGCCCTTCCTAACGTAGTGGTATGTGTCACGGTGGAAGCGGACCAGGGTC

a    G  S  A  A  G  K  D  C  I  T  I  H  S  A  T  F  A  W  S  Q  -

     GAAAGCCCTCCCTGCCTCCACAGAATAAACCTCACGGTGCCCCAGGGCTGTCTGCTGGCT
1921 ---------+---------+---------+---------+---------+---------+ 1980
     CTTTCGGGAGGGACGGAGGTGTCTTATTTGGAGTGCCACGGGGTCCCGACAGACGACCGA

a    E  S  P  P  C  L  H  R  I  N  L  T  V  P  Q  G  C  L  L  A  -

     GTTGTCGGTCCAGTGGGGGCAGGGAAGTCCTCCCTGCTGTCCGCCCTCCTTGGGGAGCTG
1981 ---------+---------+---------+---------+---------+---------+ 2040
     CAACAGCCAGGTCACCCCCGTCCCTTCAGGAGGGACGACAGGCGGGAGGAACCCCTCGAC

a    V  V  G  P  V  G  A  G  K  S  S  L  L  S  A  L  L  G  E  L  -

     TCAAAGGTGGAGGGGTTCGTGAGCATCGAGGGTGCTGTGGCCTACGTGCCCCAGGAGGCC
2041 ---------+---------+---------+---------+---------+---------+ 2100
     AGTTTCCACCTCCCCAAGCACTCGTAGCTCCCACGACACCGGATGCACGGGGTCCTCCGG

a    S  K  V  E  G  F  V  S  I  E  G  A  V  A  Y  V  P  Q  E  A  -

     TGGGTGCAGAACACCTCTGTGGTAGAGAATGTGTGCTTCGGGCAGGAGCTGGACCCACCC
```

Figure 15E

2101 ---------+---------+---------+---------+---------+---------+ 2160
ACCCACGTCTTGTGGAGACACCATCTCTTACACACGAAGCCCGTCCTCGACCTGGGTGGG

a W V Q N T S V V E N V C F G Q E L D P P -

TGGCTGGAGAGAGTACTAGAAGCCTGTGCCCTGCAGCCAGATGTGGACAGCTTCCCTGAG
2161 ---------+---------+---------+---------+---------+---------+ 2220
ACCGACCTCTCTCATGATCTTCGGACACGGGACGTCGGTCTACACCTGTCGAAGGGACTC

a W L E R V L E A C A L Q P D V D S F P E -

GGAATCCACACTTCAATTGGGGAGCAGGGCATGAATCTCTCCGGAGGCCAGAAGCAGCGG
2221 ---------+---------+---------+---------+---------+---------+ 2280
CCTTAGGTGTGAAGTTAACCCCTCGTCCCGTACTTAGAGAGGCCTCCGGTCTTCGTCGCC

a G I H T S I G E Q G M N L S G G Q K Q R -

CTGAGCCTGGCCCGGGCTGTATACAGAAAGGCAGCTGTGTACCTGCTGGATGACCCCCTG
2281 ---------+---------+---------+---------+---------+---------+ 2340
GACTCGGACCGGGCCCGACATATGTCTTTCCGTCGACACATGGACGACCTACTGGGGGAC

a L S L A R A V Y R K A A V Y L L D D P L -

GCGGCCCTGGATGCCCACGTTGGCCAGCATGTCTTCAACCAGGTCATTGGGCCTGGTGGG
2341 ---------+---------+---------+---------+---------+---------+ 2400
CGCCGGGACCTACGGGTGCAACCGGTCGTACAGAAGTTGGTCCAGTAACCCGGACCACCC

a A A L D A H V G Q H V F N Q V I G P G G -

CTACTCCAGGGAACAACACGGATTCTCGTGACGCACGCACTCCACATCCTGCCCCAGGCT
2401 ---------+---------+---------+---------+---------+---------+ 2460
GATGAGGTCCCTTGTTGTGCCTAAGAGCACTGCGTGCGTGAGGTGTAGGACGGGGTCCGA

a L L Q G T T R I L V T H A L H I L P Q A -

GATTGGATCATAGTGCTGGCAAATGGGGCCATCGCAGAGATGGGTTCCTACCAGGAGCTT
2461 ---------+---------+---------+---------+---------+---------+ 2520
CTAACCTAGTATCACGACCGTTTACCCCGGTAGCGTCTCTACCCAAGGATGGTCCTCGAA

a D W I I V L A N G A I A E M G S Y Q E L -

CTGCAGAGGAAGGGGGCCCTCGTGTGTCTTCTGGATCAAGCCAGACAGCCAGGAGATAGA
2521 ---------+---------+---------+---------+---------+---------+ 2580

Figure 15F

```
     GACGTCTCCTTCCCCCGGGAGCACACAGAAGACCTAGTTCGGTCTGTCGGTCCTCTATCT

a    L Q R K G A L V C L L D Q A R Q P G D R -

     GGAGAAGGAGAAACAGAACCTGGGACCAGCACCAAGGACCCCAGAGGCACCTCTGCAGGC
2581 ---------+---------+---------+---------+---------+---------+ 2640
     CCTCTTCCTCTTTGTCTTGGACCCTGGTCGTGGTTCCTGGGGTCTCCGTGGAGACGTCCG

a    G E G E T E P G T S T K D P R G T S A G -

     AGGAGGCCCGAGCTTAGACGCGAGAGGTCCATCAAGTCAGTCCCTGAGAAGGACCGTACC
2641 ---------+---------+---------+---------+---------+---------+ 2700
     TCCTCCGGGCTCGAATCTGCGCTCTCCAGGTAGTTCAGTCAGGGACTCTTCCTGGCATGG

a    R R P E L R R E R S I K S V P E K D R T -

     ACTTCAGAAGCCCAGACAGAGGTTCCTCTGGATGACCCTGACAGGGCAGGATGGCCAGCA
2701 ---------+---------+---------+---------+---------+---------+ 2760
     TGAAGTCTTCGGGTCTGTCTCCAAGGAGACCTACTGGGACTGTCCCGTCCTACCGGTCGT

a    T S E A Q T E V P L D D P D R A G W P A -

     GGAAAGGACAGCATCCAATACGGCAGGGTGAAGGCCACAGTGCACCTGGCCTACCTGCGT
2761 ---------+---------+---------+---------+---------+---------+ 2820
     CCTTTCCTGTCGTAGGTTATGCCGTCCCACTTCCGGTGTCACGTGGACCGGATGGACGCA

a    G K D S I Q Y G R V K A T V H L A Y L R -

     GCCGTGGGCACCCCCCTCTGCCTCTACGCACTCTTCCTCTTCCTCTGCCAGCAAGTGGCC
2821 ---------+---------+---------+---------+---------+---------+ 2880
     CGGCACCCGTGGGGGGAGACGGAGATGCGTGAGAAGGAGAAGGAGACGGTCGTTCACCGG

a    A V G T P L C L Y A L F L F L C Q Q V A -

     TCCTTCTGCCGGGGCTACTGGCTGAGCCTGTGGGCGGACGACCCTGCAGTAGGTGGGCAG
2881 ---------+---------+---------+---------+---------+---------+ 2940
     AGGAAGACGGCCCCGATGACCGACTCGGACACCCGCCTGCTGGGACGTCATCCACCCGTC

a    S F C R G Y W L S L W A D D P A V G G Q -

     CAGACGCAGGCAGCCCTGCGTGGCGGGATCTTCGGGCTCCTCGGCTGTCTCCAAGCCATT
2941 ---------+---------+---------+---------+---------+---------+ 3000
     GTCTGCGTCCGTCGGGACGCACCGCCCTAGAAGCCCGAGGAGCCGACAGAGGTTCGGTAA
```

Figure 15G

a Q T Q A A L R G G I F G L L G C L Q A I -

GGGCTGTTTGCCTCCATGGCTGCGGTGCTCCTAGGTGGGGCCCGGGCATCCAGGTTGCTC
3001 ---------+---------+---------+---------+---------+---------+ 3060
CCCGACAAACGGAGGTACCGACGCCACGAGGATCCACCCCGGGCCCGTAGGTCCAACGAG

a G L F A S M A A V L L G G A R A S R L L -

TTCCAGAGGCTCCTGTGGGATGTGGTGCGATCTCCCATCAGCTTCTTTGAGCGGACACCC
3061 ---------+---------+---------+---------+---------+---------+ 3120
AAGGTCTCCGAGGACACCCTACACCACGCTAGAGGGTAGTCGAAGAAACTCGCCTGTGGG

a F Q R L L W D V V R S P I S F F E R T P -

ATTGGTCACCTGCTAAACCGCTTCTCCAAGGAGACAGACACGGTTGACGTGGACATTCCA
3121 ---------+---------+---------+---------+---------+---------+ 3180
TAACCAGTGGACGATTTGGCGAAGAGGTTCCTCTGTCTGTGCCAACTGCACCTGTAAGGT

a I G H L L N R F S K E T D T V D V D I P -

GACAAACTCCGGTCCCTGCTGATGTACGCCTTTGGACTCCTGGAGGTCAGCCTGGTGGTG
3181 ---------+---------+---------+---------+---------+---------+ 3240
CTGTTTGAGGCCAGGGACGACTACATGCGGAAACCTGAGGACCTCCAGTCGGACCACCAC

a D K L R S L L M Y A F G L L E V S L V V -

GCAGTGGCTACCCCACTGGCCACTGTGGCCATCCTGCCACTGTTTCTCCTCTACGCTGGG
3241 ---------+---------+---------+---------+---------+---------+ 3300
CGTCACCGATGGGGTGACCGGTGACACCGGTAGGACGGTGACAAAGAGGAGATGCGACCC

a A V A T P L A T V A I L P L F L L Y A G -

TTTCAGAGCCTGTATGTGGTTAGCTCATGCCAGCTGAGACGCTTGGAGTCAGCCAGCTAC
3301 ---------+---------+---------+---------+---------+---------+ 3360
AAAGTCTCGGACATACACCAATCGAGTACGGTCGACTCTGCGAACCTCAGTCGGTCGATG

a F Q S L Y V V S S C Q L R R L E S A S Y -

TCGTCTGTCTGCTCCCACATGGCTGAGACGTTCCAGGGCAGCACAGTGGTCCGGGCATTC
3361 ---------+---------+---------+---------+---------+---------+ 3420
AGCAGACAGACGAGGGTGTACCGACTCTGCAAGGTCCCGTCGTGTCACCAGGCCCGTAAG

Figure 15H

```
a      S  S  V  C  S  H  M  A  E  T  F  Q  G  S  T  V  V  R  A  F  -

       CGAACCCAGGCCCCTCTTGTGGCTCAGAACAATGCTCGCGTAGATGAAAGCCAGAGGATC
  3421 ---------+---------+---------+---------+---------+---------+  3480
       GCTTGGGTCCGGGGAGAACACCGAGTCTTGTTACGAGCGCATCTACTTTCGGTCTCCTAG

a      R  T  Q  A  P  L  V  A  Q  N  N  A  R  V  D  E  S  Q  R  I  -

       AGTTTCCCGCGACTGGTGGCTGACAGGTGGCTTGCGGCCAATGTGGAGCTCCTGGGGAAT
  3481 ---------+---------+---------+---------+---------+---------+  3540
       TCAAAGGGCGCTGACCACCGACTGTCCACCGAACGCCGGTTACACCTCGAGGACCCCTTA

a      S  F  P  R  L  V  A  D  R  W  L  A  A  N  V  E  L  L  G  N  -

       GGCCTGGTGTTTGCAGCTGCCACGTGTGCTGTGCTGAGCAAAGCCCACCTCAGTGCTGGC
  3541 ---------+---------+---------+---------+---------+---------+  3600
       CCGGACCACAAACGTCGACGGTGCACACGACACGACTCGTTTCGGGTGGAGTCACGACCG

a      G  L  V  F  A  A  A  T  C  A  V  L  S  K  A  H  L  S  A  G  -

       CTCGTGGGCTTCTCTGTCTCTGCTGCCCTCCAGGTGACCCAGGCACTGCAGTGGGTTGTT
  3601 ---------+---------+---------+---------+---------+---------+  3660
       GAGCACCCGAAGAGACAGAGACGACGGGAGGTCCACTGGGTCCGTGACGTCACCCAACAA

a      L  V  G  F  S  V  S  A  A  L  Q  V  T  Q  A  L  Q  W  V  V  -

       CGCAACTGGACAGACCTAGAGAACAGCATCGTGTCAGTGGAGCGGATGCAGGACTATGCC
  3661 ---------+---------+---------+---------+---------+---------+  3720
       GCGTTGACCTGTCTGGATCTCTTGTCGTAGCACAGTCACCTCGCCTACGTCCTGATACGG

a      R  N  W  T  D  L  E  N  S  I  V  S  V  E  R  M  Q  D  Y  A  -

       TGGACGCCCAAGGAGGCTCCCTGGAGGCTGCCCACATGTGCAGCTCAGCCCCCCTGGCCT
  3721 ---------+---------+---------+---------+---------+---------+  3780
       ACCTGCGGGTTCCTCCGAGGGACCTCCGACGGGTGTACACGTCGAGTCGGGGGGACCGGA

a      W  T  P  K  E  A  P  W  R  L  P  T  C  A  A  Q  P  P  W  P  -

       CAGGGCGGGCAGATCGAGTTCCGGGACTTTGGGCTAAGATACCGACCTGAGCTCCCGCTG
  3781 ---------+---------+---------+---------+---------+---------+  3840
       GTCCCGCCCGTCTAGCTCAAGGCCCTGAAACCCGATTCTATGGCTGGACTCGAGGGCGAC

a      Q  G  G  Q  I  E  F  R  D  F  G  L  R  Y  R  P  E  L  P  L  -
```

Figure 15I

```
     GCTGTGCAGGGCGTGTCCCTCAAGATCCACGCAGGAGAGAAGGTGGGCATCGTTGGCAGG
3841 ---------+---------+---------+---------+---------+---------+ 3900
     CGACACGTCCCGCACAGGGAGTTCTAGGTGCGTCCTCTCTTCCACCCGTAGCAACCGTCC

a     A  V  Q  G  V  S  L  K  I  H  A  G  E  K  V  G  I  V  G  R  -

     ACCGGGGCAGGGAAGTCCTCCCTGGCCAGTGGGCTGCTGCGGCTCCAGGAGGCAGCTGAG
3901 ---------+---------+---------+---------+---------+---------+ 3960
     TGGCCCCGTCCCTTCAGGAGGGACCGGTCACCCGACGACGCCGAGGTCCTCCGTCGACTC

a     T  G  A  G  K  S  S  L  A  S  G  L  L  R  L  Q  E  A  A  E  -

     GGTGGGATCTGGATCGACGGGGTCCCCATTGCCCACGTGGGGCTGCACACACTGCGCTCC
3961 ---------+---------+---------+---------+---------+---------+ 4020
     CCACCCTAGACCTAGCTGCCCCAGGGGTAACGGGTGCACCCCGACGTGTGTGACGCGAGG

a     G  G  I  W  I  D  G  V  P  I  A  H  V  G  L  H  T  L  R  S  -

     AGGATCAGCATCATCCCCCAGGACCCCATCCTGTTCCCTGGCTCTCTGCGGATGAACCTC
4021 ---------+---------+---------+---------+---------+---------+ 4080
     TCCTAGTCGTAGTAGGGGGTCCTGGGGTAGGACAAGGGACCGAGAGACGCCTACTTGGAG

a     R  I  S  I  I  P  Q  D  P  I  L  F  P  G  S  L  R  M  N  L  -

     GACCTGCTGCAGGAGCACTCGGACGAGGCTATCTGGGCAGCCCTGGAGACGGTGCAGCTC
4081 ---------+---------+---------+---------+---------+---------+ 4140
     CTGGACGACGTCCTCGTGAGCCTGCTCCGATAGACCCGTCGGGACCTCTGCCACGTCGAG

a     D  L  L  Q  E  H  S  D  E  A  I  W  A  A  L  E  T  V  Q  L  -

     AAAGCCTTGGTGGCCAGCCTGCCCGGCCAGCTGCAGTACAAGTGTGCTGACCGAGGCGAG
4141 ---------+---------+---------+---------+---------+---------+ 4200
     TTTCGGAACCACCGGTCGGACGGGCCGGTCGACGTCATGTTCACACGACTGGCTCCGCTC

a     K  A  L  V  A  S  L  P  G  Q  L  Q  Y  K  C  A  D  R  G  E  -

     GACCTGAGCGTGGGCCAGAAACAGCTCCTGTGTCTGGCACGTGCCCTTCTCCGGAAGACC
4201 ---------+---------+---------+---------+---------+---------+ 4260
     CTGGACTCGCACCCGGTCTTTGTCGAGGACACAGACCGTGCACGGGAAGAGGCCTTCTGG

a     D  L  S  V  G  Q  K  Q  L  L  C  L  A  R  A  L  L  R  K  T  -
```

Figure 15J

```
     CAGATCCTCATCCTGGACGAGGCTACTGCTGCCGTGGACCCTGGCACGGAGCTGCAGATG
4261 ---------+---------+---------+---------+---------+---------+ 4320
     GTCTAGGAGTAGGACCTGCTCCGATGACGACGGCACCTGGGACCGTGCCTCGACGTCTAC

a    Q I L I L D E A T A A V D P G T E L Q M -

     CAGGCCATGCTCGGGAGCTGGTTTGCACAGTGCACTGTGCTGCTCATTGCCCACCGCCTG
4321 ---------+---------+---------+---------+---------+---------+ 4380
     GTCCGGTACGAGCCCTCGACCAAACGTGTCACGTGACACGACGAGTAACGGGTGGCGGAC

a    Q A M L G S W F A Q C T V L L I A H R L -

     CGCTCCGTGATGGACTGTGCCCGGGTTCTGGTCATGGACAAGGGGCAGGTGGCAGAGAGC
4381 ---------+---------+---------+---------+---------+---------+ 4440
     GCGAGGCACTACCTGACACGGGCCCAAGACCAGTACCTGTTCCCCGTCCACCGTCTCTCG

a    R S V M D C A R V L V M D K G Q V A E S -

     GGCAGCCCGGCCCAGCTGCTGGCCCAGAAGGGCCTGTTTTACAGACTGGCCCAGGAGTCA
4441 ---------+---------+---------+---------+---------+---------+ 4500
     CCGTCGGGCCGGGTCGACGACCGGGTCTTCCCGGACAAAATGTCTGACCGGGTCCTCAGT

a    G S P A Q L L A Q K G L F Y R L A Q E S -

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4501 ---------+-- 4512
     CCGGACCAGACT

a    G L V * -
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Figure 15K

SEQUENCE LISTING

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Leu Val Phe Tyr Val Leu Val Asn Ser Ser Gln Thr Leu His Asn Lys
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Met Phe Glu Ser Ile Leu Lys Ala Pro Val Leu Phe Phe Asp Arg Asn
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Pro Ile Gly Arg Ile Leu Asn Arg Phe Ser Lys Asp Ile Gly His Leu
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Asp Asp Leu Leu Pro Leu Thr Phe Leu Asp Phe Ile Gln Thr Leu Leu
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Gln Val Val Gly Val Val Ser Val Ala Val Ala Val Ile Pro Trp Ile
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Tyr Phe Leu Glu Thr Ser Arg Asp Val Lys Arg Leu Glu Ser Thr Thr
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Ala His Gln Asp Leu His Ser Glu Ala Trp Phe Leu Phe Leu Thr Thr
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Phe Gln Trp Cys Val Arg Gln Ser Ala Glu Val Glu Asn Met Met Ile
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Val Leu Lys His Leu Thr Ala Leu Ile Lys Ser Gln Glu Lys Val Gly
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Pro Phe Lys Glu His Thr Asp Glu Glu Leu Trp Asn Ala Leu Arg Glu
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Val Gln Leu Lys Glu Thr Ile Glu Asp Leu Pro Gly Lys Met Asp Thr
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Val Cys Leu Ala Arg Ala Ile Leu Arg Lys Asn Gln Ile Leu Ile Ile
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Ala Ala Ala Leu Thr Glu Thr Ala Lys Gln Val Tyr Phe Lys Arg Asn
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Tyr Pro His Ile Gly His Thr Asp His Met Val Thr Asn Thr Ser Asn
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Ala Leu Glu Thr Ala Ala Arg Ala Glu Gly Leu Ser Leu Asp Ala Ser

50 55 60
Met His Ser Gln Leu Arg Ile Leu Asp Glu Glu His Pro Lys Gly Lys
65 70 75 80
Tyr His His Gly Leu Ser Ala Leu Lys Pro Ile Arg Thr Thr Ser Lys
85 90 95
His Gln His Pro Val Asp Asn Ala Gly Leu Phe Ser Cys Met Thr Phe
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Ser Trp Leu Ser Ser Leu Ala Arg Val Ala His Lys Lys Gly Glu Leu
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Ser Met Glu Asp Val Trp Ser Leu Ser Lys His Glu Ser Ser Asp Val
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Asn Cys Arg Arg Leu Glu Arg Leu Trp Gln Glu Glu Leu Asn Glu Val
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Gly Pro Asp Ala Ala Ser Leu Arg Arg Val Val Trp Ile Phe Cys Arg
165 170 175
Thr Arg Leu Ile Leu Ser Ile Val Cys Leu Met Ile Thr Gln Leu Ala
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Gly Phe Ser Gly Pro Ala Phe Met Val Lys His Leu Leu Glu Tyr Thr
195 200 205
Gln Ala Thr Glu Ser Asn Leu Gln Tyr Ser Leu Leu Leu Val Leu Gly
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225 230 235 240
Ala Leu Asn Tyr Arg Thr Gly Val Arg Leu Arg Gly Ala Ile Leu Thr
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Glu Ala Ala Ala Val Gly Ser Leu Leu Ala Gly Gly Pro Val Val Ala
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Ser Arg Leu Thr Ala Tyr Phe Arg Arg Lys Cys Val Ala Ala Thr Asp
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Ser Asp Leu Thr Glu Ile Gly Glu Arg Gly Ala Asn Leu Ser Gly Gly
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Gln Arg Gln Arg Ile Ser Leu Ala Arg Ala Leu Tyr Ser Asp Arg Ser
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Asn His Ile Phe Asn Ser Ala Ile Arg Lys His Leu Lys Ser Lys Thr
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Val Leu Phe Val Thr His Gln Leu Gln Tyr Leu Val Asp Cys Asp Glu
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Val Ile Phe Met Lys Glu Gly Cys Ile Thr Glu Arg Gly Thr His Glu
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Glu Leu Met Asn Leu Asn Gly Asp Tyr Ala Thr Ile Phe Asn Asn Leu
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Leu Leu Gly Glu Thr Pro Pro Val Glu Ile Asn Ser Lys Lys Glu Thr
785                     790                     795                 800
Ser Gly Ser Gln Lys Lys Ser Gln Asp Lys Gly Pro Lys Thr Gly Ser
                805                     810                     815
Val Lys Lys Glu Lys Ala Val Lys Pro Glu Glu Gly Gln Leu Val Gln
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Tyr Ile Gln Ala Ala Gly Gly Pro Leu Ala Phe Leu Val Ile Met Ala
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Lys Asp Met Asp Glu Val Asp Val Arg Leu Pro Phe Gln Ala Glu Met
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Ser Ile Gln Gly Leu Ala Thr Ile His Ala Tyr Asn Lys Gly Gln Glu
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Pro Asp Trp Pro Gln Glu Gly Glu Val Thr Phe Glu Asn Ala Glu Met
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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US99/06644

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) :A01N 63/00, A61K 39/395, C12N 15/00, A01N 61/00, C07H 21/02
US CL :Please See Extra Sheet.
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 424/93.1, 93.2, 130.1; 435/320.1, 325; 514/1; 536/23.1; 800/13, 18

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, STN, MEDLINE, BIOSIS, CAPLUS, SCISEARCH

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Database GENBANK, Accession No. U66687, ALLIKMETS et al. Characterization of the human ABC superfamily: isolation and mapping of 21 new genes using the expressed sequence tags databases. Hum. Mol. Genet. 5(10), pp. 1649-1655, 26 March 1997.	21
X	Database GENBANK, Accesion No. D77412, NISHIGUCHI. S. et al., A catalogue of genes in mouse embryonal carcinoma F9 cells identified with expressed sequence tags. J. Biochem. 119 (4), pp. 749-767, 04 October 1996.	22

[X] Further documents are listed in the continuation of Box C. [ ] See patent family annex.

* Special categories of cited documents:

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
20 MAY 1999	01 JUL 1999

Name and mailing address of the ISA/US
Commissioner of Patents and Trademarks
Box PCT
Washington, D.C. 20231
Facsimile No. (703) 305-3230

Authorized officer
SHIN-LIN CHEN
Telephone No. (703) 308-0196

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US99/06644

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT		
Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	Database GENBANK, Accession No. U66674, ALLIKMETS, R. et al., Characterization of the human ABC superfamily: isolation and mapping of 21 new genes using the expressed sequence tags database. Hum. Mol. Genet.16 March 1997, 5 (10), pp. 1649-1655.	33
X	Database GENBANK, Accession No. R97754, HILLIER, L. et al., The WashU-Merk EST project. 11 September 1995.	44
Y	KOIKE et al. A Canalicular Multispecific Organic Anion Transporter (cMOAT) Antisense cDNA Enhances Drug Sensitivitiy in Human Hepatic Cancer Cells. Cancer Research. 15 December 1997, Vol. 57, No. 24, pages 5475-5479, see entire document.	55-57
A,P	LEE et al. Isolation of MOAT-B, a Widely Expressed Multidrug Resistance-associated Proteins Canalicular Multispecific Organic Anion Transporter-related Transporter. Cancer Research. 01 July 1998, Vol 58, No. 13, pages 2741-2747, see entire document.	1-58
A,P	BELINSKY et al. Characterization of MOAT-C and MOAT-D, New Nembers of the MRP/cMOAT Subfamily of Transporter Proteins. Natl. Cancer Inst. 18 November 1998, Vol 90, No. 22, pages 1735-1741.	1-58
A	SUZUKI et al. Excretion of GSSG and Glutathione Conjugates Mediated by MRP1 and cMOAT/MRPS. Seminars in Liver Disease. 1998, Vol 18, No. 4, pages 359-376.	1-58

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US99/06644

A. CLASSIFICATION OF SUBJECT MATTER:
US CL :

424/93.1, 93.2, 130.1; 435/320.1, 325; 514/1; 536/23.1; 800/13, 18